03/99/628 508/1051-7

(MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Fri Jun 11 17:13:56 1999; MasPar time 4.85 Seconds 65.804 Million cell updates/sec

Description: Perfect Score: >US-08-991-628-1 (1-15) from US08991628.pep 101

ATQKITYRISGVGID 15

Scoring table:

Sequence:

PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Pont-processing: Minimum Match 0% Listing first 45 summaries

Database:

-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part33 33:part33
34:part24 35:part35 36:part36 37:part37 38:part38

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Statistics:

Mean 18.436;

Variance 54.674;

scale 0.337

SUMMARIES

Result No.	Score	Query Match	Length	80	IJ	Description	Pred. No
, <u></u>	101	100.0	15	20	W04841	Self epitope of desmo	1.83e-04
2	101	100.0	614	19	W07908	Š	1.83e-04
w	101	100.0	999	σ	R30742	Human pemphiqus vulga	1.83e-04
4	87	86.1	778	21	W15489	Pemphiqus foliaceus a	9.69e-03
5	57	56.4	1363	27	W31706	Bovine coronavirus E2	2.94e+01
6	57	56.4	1363	N	R11061	Bovine Coronavirus E2	2.94e+01
7	54	53.5	878	15	R85487	Human E-cadherin prec	6.20e+01
8	54	53.5	878	10	R55060	Sequence of human liv	6.20e+01
9	53	52.5	309	ب	R06441	MG-6 antigen.	7.93e+01
10	52	51.5	626	30	W37140	Pea plastidial phosph	1.01e+02
11	51	50.5	504	3 8	W73500	Trabecular meshwork i	1.29e+02
12	51	50.5	504	39	W89391	Human trabecular mesh	1.29e+02
13	51	50.5	504	34	W64669	Human TIGR protein.	1.29e+02
14	51	50.5	504	ű	W60670	Human glaucoma associ	1.29e+02
15	51	50.5	504	<u>ω</u>	W70496	Trabecular meshwork i	1.29e+02
16	51	50.5	560	24	W13009	Spompot of desmosomal	1.29e+0

17		>	x	u	<u>د</u>	Conce encoded by	S
18	51	50.5	916	21	W13129	ngth human	
61			\vdash	24	2565	an cadherin-4.	.29e+
20		0	80	36	948	utinin	.29e+
21			œ	17	602	haemag	.29e+
22		.0	35	36	949	utinin	.29e+
23		٥.	35	17	603	valis hagD h	.29e+
24		0	56	هــــو	414	oris proteina	.29e+
5		0	95	2	56	utant protease (del	. 29
6		.0	96	N	055	(A13	.29e+
27		.0	96	N	055	t protease (Al3	.29e+
æ		0	96	N	950	e (K13	. 29e
9		0	96	N	055	ant protease (Al3	. 29
õ		0	96	N	056	nt protease (. 29e
ĩ		0	96	N	056	ant protease (K74	. 29e
ຄ		0	96	N	094	t protease (del	. 29
ü		0	97	N	4	se (del	. 29e
34		9	23	29	670	on peptid	
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8		9	4	37	4	Fragment of human sec	.64e+
37		9	4	N	097	Acetoacetyl CoA reduc	
8		9	*	بر	P94157	redu	1.64e+0
9		9	4	σ	3219	ce encoded by	
0		9	329	13	32	-CoA-redu	1.64e+0
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r-cells in individuals with the autoimmune disease. This peptide is derived from the human desmoglein 3 protein (amino acids 78-93 (sic)) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein protein are described in W04841-47. Sequence 15 AA;	/42. And the series of other self; sease 38; 58pp; Engli; preparations from the self; preparations from the self; preparation from the self; r an isolated high to the their self or spending to a se	W04841; W04841; W04841; 18-FEB-1997 (first entry) Self epitope of desmoglein 3, implicated in autoimmune disease. Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; emphigus vulgaris; desmoglein; multiple sclerosis; herpes simplex virus; adenovirus; phosphomannomutase; human papillomavirus; Epstein-Barr virus; DNA polymerase; influenza; haemagglutinin; reovirus; bNA polymerase; HOMO sapiens. W09627387-Al. 12-SEP-1996. 07-MAR-1995; U03182. 07-MAR-1995; U03182. 07-MAR-1995; U03182. 07-MAR-1995; U03182. Strominger JL, Wucherpfennig KW;

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detection;

fusion

protein.

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Query Match
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris (laim 1; Page 7-9; 9pp; Japanese. W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgGl hinge region and the resulting fusion protein is useful to treat or diagnose sequence 614 AA;
                                                                                                   DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.
This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
                                                                                                                                                                                                                                                N-PSDB; Q35992.
                                                                                                                                                                                                                                                                                    27-NOV-1991; 798918.
27-NOV-1991; US-798918.
(USSH) US DEPT HEALTH &
Amagai M, Klaus-kovtun V
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J08188540-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
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JS7798918-A.
                                                                                                                                                                                                                                                                                                                                                                                                                      ceratinocyte cell surface antigen; glycoprotein;
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93-067436/08.
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ody; immunoglobulin G; IgGl; fusion protein; diagnosis;
; pemphigus vulgaris; PV; bulla; blister; skin disease;
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V, Stanley JR;
    Score 101;
Pred. No. 1.
0; Mismatc
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    re 101; DB 6; Le
1. No. 1.83e-04;
Mismatches '0;
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.83e-04;
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                                           Length
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Chis sequence represents a fused protein recognised by pemphigus follaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus follaceus is antigen protein through the hinge portion. Pemphigus follaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus follaceus antigen fusion protein is useful to treat pemphigus follaceus. The antigen is especially administered through an adorbent upon which the fusion protein is immobilised via a carrier. The fusion protein is also useful for detecting pemphigus follaceus antibodies which is useful infumunocalismosis. The fusion protein has little or no side effects.
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Best Local S
Matches 1
                                     US5672350-A.
30-SEP-1997.
22-AUG-1989;
19-DEC-1991;
22-AUG-1989;
18-OCT-1991;
                                                                                                                                                                                                                                                                                                                                            BCV;
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Pemphigus foliaceus antigen-IgG constant region;
Pemphigus foliaceus; autoantibody; constant region;
Pemphigus foliaceus; autoantibody; constant region;
extracellular region; antigen; hinge portion; skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in immunodiagnosis. Sequence 778 AA;
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WPI; 97-241758/22.
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L2-SEP-1995;
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2 protein; peplomer
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  VETERINARY INFECTIOUS DISEASE
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US-397689.
US-779500.
US-171763.
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larity 80.0%;
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d. No. 9.69e-03;
Mismatches 2;
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10-AUG-1990; CA0252.
22-AUG-1989; US-397689.
(VETE-) VETERINARY INFECTIO.
Parker MD, Cox GJ, Babiuk LA;
WPI, 91-087247/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9102752-A.
                                                                                                                                                                                             E3 - useful as vaccine component Disclosure; Fig 3 (1-6); 70pp; English.
Disclosure; Fig 3 (1-6); 70pp; English.
E2 protein is one of the four proteins (N, E1, E2 and E E2 protein E2 and E3 polypeptides, or fragments of these subunit antigens in vaccines for protection against or BCV, without risk of infection.
Sequence 1363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~4-mAY-1991 (first entry)
Bovine Coronavirus E2 protein.
Bovine Coronavirus; BCV; E2; E
Bovine coronavirus - Quebec is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R11061;
24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R11061 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coronavirus polypeptide(s)
Claim 13; Fig 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Deoxyribonucleic acid encoding Bovine
E3 - useful as vaccine component
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q10947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; T89387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babiuk LA, Cox GJ,
WPI; 97-488823/45.
                                                       995
                               nvqyringigv 1005
:: |||:|:|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KITYRISGVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nvqyringigv 1005
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     KITYRISGVGI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 56.4%;
Similarity 45.5%;
5; Conservative
                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1363 AA;
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- sig_peptide
766..766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  us; BCV; E2; E3; vac
us - Quebec isolate
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 1363
                                                                                                                              56.4%;
45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "probable cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane_domain
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Pred.
5; M
                                                                                                                           Score
Pred.
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1. No. 2.94e+01;
Mismatches 1;
                                                                                                   e 57; DB 2; Le
. No. 2.94e+01;
Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine.
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                                                                                                                                                     Length 1363;
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                                                                                                   Indels
                                                                                                                                                                                                                                                       ameliorating
                                                                                                                                                                                                                                                                              are
                                                                                                                                                                                                                                                                            composing are used as
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                                                                                                   Gaps
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RESULT

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TRESULT RESULT R
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(WYYA) UNIV YALE.

MOTTOW JS, Rimm DL;

R WPI; 94-183426/22.

R N-PSDB; Q65487.

Purified human E-cadherin protein and nucleic acid - uperfied human E-cadherin for diagnosis, prognosis, therapy and protein it cadherin is a cell adhesion molecule that is also k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                             Disclosure; Page 70-75; 103pp; English.

The human E-cadherin protein precursor (R85487) is expressed by an cDNA clone (T05764) derived from human liver. The extracellular an cDNA clone (T05764) derived from human liver. The extracellular domain of E-cadherin is used to generate peptides that specifically bind to heterotypic cognates of E-cadherin and which inhibit adhesion of intra-epithelial T-lymphocytes to E-cadherin-expressing epithelial or endothelial cells in vitro or invo, thereby modulating mucosal immune responses. Such peptides are also specifically reactive with a monoclonal antibody (E4.6 or E6.1) that binds to E-cadherin and that can inhibit T-cell binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human E-cadherin precursor.
E-cadherin; T-lymphocyte; alpha-E,beta-7 integrin; autoimmune disease; Crohn disease; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R85487
R85487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R55060 standard;
R55060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1994; US-237919.
(BGHM ) BRIGHAM & WOMENS
Brenner MB, Cepek KL;
WPI; 95-392921/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-1995;
03-MAY-1994;
                                                                                                                                                                                                                                          16-NOV-1993;
17-NOV-1992;
                                                                                                                                                                                                                                                                                          26-MAY-1994.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
WO9411401-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolating agents psoriasis, etc
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09-NOV-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 53.5%;
Similarity 100.0%;
7; Conservative
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878 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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6.20e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-cadherin -
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                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .g. Crohn's disease
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                                                                                              used to prophylaxis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uvomorulin, L-CAM and Cell CAM 120/80. The DNA encoding hEC was obtd. by screening normal human liver and hepatocellular carcinoma cDNA clibraries and a colonic epithelial cell cDNA library. The following sequences are specifically claimed: AAS 1-878; 131-878; 30 sequential AAS from AAS 308-878; AAS 1-150; AAS 178-289; AAS 290-401; AAS 402-513; AAS 178-513; AAS 151-703; AAS 17-703; AAS 728-878; CAAS 704-878; nucleotide sequences comprising nucleotide numbers 116-2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-1648; 384-1208; 641-2046; 685-1335; 880-1661; 1199-1742; 1373-1742; C1705-2204; 2458-2775; DNA encoding at least 30 AAS selected from AAS 308-878. The prods. can be used in the diagnosis, prognosis, therapy and prophylaxis of conditions involving improper E-cadherin expression. Suitable dosages for i.v. admin. of a protein are 50-500 mcg/kg body wt.
                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local s
Matches
03-JUL-1997;
10-FEB-1997;
09-JUL-1996;
18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                     plagnostic and vaccine for poultry mycoplasma serum - utilises antigen protein of the disease and recombinant vector incorporated with its coding gene.

Claim 2; Fig 1f; 20pp; Japanese.

DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be lighted to other DNA to produce fusion proteins with an N-terminal
                                                                       rug3 mutation.
Pisum sativum var.
WO9801574-A1.
                                                                                                                                                                                                                                                                                                                                                 bacterial enzyme sequence. See also R05081-2 and R06437-40. Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MG-6
                                                                                                                             06-JUL-1998 (
                                                                                                                                                           W37140;
                                                                                                                                                                      W37140 standard; Protein; 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q05653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JAPG) Nippon Zeon KK, (SHIO)
WPI; 90-169109/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1989; 136343.
02-JUN-1989; JP-136343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma gallisepticum; poultry; vaccine 702111795-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R06441;
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                                                         L5-JAN-1998.
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                                                                                                                                                                                                                                 TOKITYRISGYG
                                                                                                               noglucomutase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                       h 52.5%;
Similarity 58.3%;
7; Conservative
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Similarity 100.0%;
7; Conservative
; E03613.
; GB-002653.
; US-021410.
; GB-015103.
                                                                                                                             (first entry)
al phosphoglucomutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                  13
                                                                                    Novella
                                                                                                               pea;
                                                                                                               PGM(p);
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Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                       Score 53; DB 1; Len
Pred. No. 7.93e+01;
3; Mismatches 2;
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                                                                                                               sucrose;
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                                                                                                                                                                                                                                                                                                                    Length 309
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TOKITYRISGVGID

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                                                                                                                                                                        glaucoma (Column 25-28; 22pp; English. Claim 1; Column 25-28; 22pp; English. This sequence represents the human Trabecular meshwork induced glucocorticoid response (TIGR) protein. The TIGR protein is a secretory protein specifically bound by the antibody of the invention. The antibody, especially in labelled form, can be used in the diagnosis of glaucoma by detecting elevated levels of the protein in the trabecular meshwork of the eye. Using the antibody, glaucoma is detected more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pea seeds lacking plastidial phosphoglucomutase activity - have higher sucrose levels at end of vining period and can be vined over extended period compared to conventional varieties Disclosure; Page 58-62; 83pp; English.

This protein comprises pea plastidial phosphoglucomutase (PGM(p)), an enzyme that catalyses the interconversion of glucose-1-phosphate and glucose-6-phosphate, and is thus involved in starch synthesis. The amino acid sequence was deduced from an isolated cDNA clone (see, V00731) and shows considerable homology to known PGM sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides pea plants that have substantially reduced PGM(p) activity or which substantially lack PGM(p) activity. This may be the result of antisense or sense suppression technology. Pea seeds from such plants have higher sucrose levels at the end of the vining period and may be vined over an extended period compared to conventional varieties. The invention provides pea seeds having a sucrose content of over 6% of total weight, and a ratio of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harrison CJ, Hedle WPI; 98-101065/09. N-PSDB; V00731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
Huang W, Nguyen TD, Polansky
WPI: 99-069807/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1996; US-645900.
03-NOV-1994; US-336235.
20-OCT-1995; US-546568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sucrose content to start content of over 10. Sequence 626 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999 (first entry)
Trabecular meshwork induced glucocorticoid response protein
TIGR protein; trabecular meshwork induced glucocorticoid res
                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998.
14-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5849879-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secretory protein; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W73500 standard;
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h 50.5%;
Similarity 57.1%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              to trabecular meshwork protein -
                                                                                                                     504 AA;
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Pred. No. 1.01e+02;
2; Mismatches 2;
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e 51; DB 38; Lo
. No. 1.29e+02;
Mismatches 6;
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PT New isolated glaucoma-associated nucleic acids - which encode
PT Trabecular Meshwork Induced Glucocorticoid Response protein, used to
PT develop products for diagnosing glaucoma-related diseases
Claim 1; Fig 1; 22pp; English.
CC The present sequence is a human secretory protein from clone II.2.
CC The present sequence is a human secretory protein shighly induced by
CC Glucocorticoid Response) protein. The protein is highly induced by
CC glucocorticoid Response) protein in the protein shighly induced by
CC glucocorticoid Response) protein and proteins can be used as markers
CC for the diagnosis of glaucoma, primary open angle glaucoma (POAG),
CC gigmentary glaucoma, and low tension glaucoma and their related
CC diseases. They can also be used to diagnose or protect an individual's
CC sensitivity to elevated intraocular pressure upon administration of
CC steroids such as glucocorticoids or corticosteroids. These products can
CC also be used for diagnosing other diseases or conditions that affect the
CC expression or activity of the protein. The products can also be
CC formulated for administration to patients.
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Best Local S
Matches
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WPI; 99-095006/08.
N-PSDB; V81910.
New isolated glaucoma
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17-MAX-1996; US-649432.
03-NOV-1994; US-336235.
20-CCT-1995; US-546568.
25-JUN-1997; US-882238.
(REGC ) UNIV CALIFORNIA.
products for diagnosis, prognosis and treatment of glaucoma Claim 48; Fig 8; 105pp; English.

This sequence represents a novel human trabecular meshwork induced glucocorticoid response protein (TIGR) which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can also be used to diagnose glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human trabecular meshwork induced glucocorticoid response protein.
Human; trabecular meshwork induced glucocorticoid response protein;
TIGR; glaucoma; primary open angle glaucoma; POAG; pigmentary glaucoma;
low tension glaucoma; intraocular pressure; steroid; corticosteroid.
                                                                                                                                                                                    N-PSDB; V51391.
Use of TIGR nucleic acid
                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA Chen H, Chen P, Nguyen WPI; 98-427946/36.
                                                                                                                                                                                                                                                                                      30-JUL-1998.
09-JAN-1998; U00468.
09-SEP-1997; US-938669.
28-JAN-1997; US-791154.
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
W09832850-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TIGR protein.
TIGR; trabecular meshwork induced
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US5854415-A.
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08-мак-1999
                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; glaucoma;
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larity 57.1%;
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Pred. No. 1.29e+02;
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PD 14-MAY-1998.

PP 107-NOV-1997; U20702.

PF 21-MAR-1997; US-822999.

PR 21-MAR-1997; US-791347.

PR 30-JAN-1997; US-791347.

PR 30-JAN-1997; US-791347.

PA (IOWA) UNIV IOWA RES FOUND.

PI Alward WIM, Sheffield V, Stone EM;

PI Products to determine whether a subject has, or is at risk of, products to determine whether a subject has, or is at risk of, products to determine whether a subject has, or is at risk of, products to determine whether a subject has, or is at risk of, products to determine whether a subject has, or is at risk of, products to determine whether a subject has, or is at risk of, products to determine whether a subject has, or is at risk of, products to determine whether a subject has, or is at risk of, products to determine whether a subject has, or is at risk for identifying molecules can be used for the development of assays for identifying molecules that modulate cor protein wouldators may be an antibody, protein peptide or peptidomimetic or a nucleic acid, e.g. antisense sequence, ribozyme or cor protein wouldators may be an antibody, protein, peptide or tiple helix forming nucleic acid, e.g. antisense sequence, ribozyme or cor cor protein wouldators may be an antibody, protein, peptide or condition. Derivatives of GLClA gene can be considered to detect lesions of the condition. Derivatives of GLClA gene can be cor protein products with or to allacoma.
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W70496;
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Human glaucoma associated
Glaucoma; GLCIA; treatment
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                                                                                                                   Trabecular meshwork induced glucocorticoid response* protein Trabecular meshwork induced glucocorticoid response*; TIGR*;
                                                                                                                                                                                                                                                                                                                                                           or predisposition Sequence 504 AA;
                                                            Peptide
                                                                           Key
                                                                                         Homo sapiens
                                                                                                        human;
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                                                                                                       glaucoma;
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Similarity 57.1%;
8; Conservative
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llarity 57.1%;
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treatment; mutant; juve
                                                                                                     diagnosis
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                                                                                                                                                                                                                                                                                                e 51; DB 32; L
. No. 1.29e+02;
Mismatches 6;
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1.29e+02;
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Modified_site

Mat_protein

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New protein induced in trabecular meshwork cells by glucocorticoids

"useful in the diagnosis of glaucoma and related diseases
Sclaim 1; Fig 1A-C; 53pp; English.
CHAIN 1; Fig 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1998.
07-APR-1997; U05801.
01-APR-1997; WO-U05391.
(REGC ) UNIV CALIFORNIA.
Huang W. Nguyen TD, Polansky JR;
WPI; 98-542701/46.
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                                                               improved methods and reagents for diagnosing glaucoma and related disorders, such as cardiovascular and immunological diseases that disorders, such as cardiovascular and immunological diagnosing glaucoma affect expression of TIGR*. A claimed method of diagnosing glaucoma involves determining if the amount of TIGR* present in the HTM exceeds the amount found in an individual not predisposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V33484.
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Query Match Best Local Similarity

50.5%; 57.1%;

Score 51; DB 36; Length 504; Pred. No. 1.29e+02;

Db 281 tgettwridtvgtd 294 || || || || | Qy 2 TQKITYRISGVGID 15

Matches

8

Conservative

0

Mismatches

6;

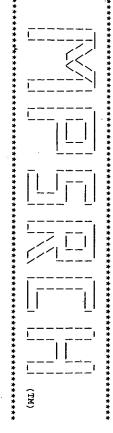
Indels

0;

Gaps

0;

Search completed: Fri Jun 11 17:15:46 1999 Job time : 110 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:12:13 1999; MasPar time 4.23 Seconds 142.091 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-991-628-1 (1-15) from US08991628.pep 101 1 ATQKITYRISGVGID 15

Scoring table:

PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 25.979; Variance 34.700; scale 0.749

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 4 4 4 4 4 7 7 6 6 7 7 11 11 11 11 11 11 11 11 11 11 11 11	Result
101 87 57 57 57 57 57 57 57 57 57 57 57 57 57	score
100 0 86.11 57.4 56.4 56.4 56.4 56.4 56.4 56.4 56.4 56	Query Match
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IJHUG3 IJHOG1 IJHOG1 E70367 T01000 VG1H0M S44241 VG1HCP VG1HCP VG1HYA D70163 S173495 S593495 S593495 S593495 S593495 S593495 S17349 S1734	Ħ
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative

Score 101; DB 1; Length 999; Pred. No. 4.47e-10; 0; Mismatches 0; Indels

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VGIH59	H71379	JC4554	S68865	S65159	JQ1534	VGIHJ2	A37474	S29998	JQ2168	VGIHMJ	D7:1416	H71409	A30481	A49307	A47485	B47485		511		I51134	534438
rote	probable tpr protein	ABC-type transporter	fimbrial protein hifE	thetical pro		E2 glycoprotein precu	surface glycoprotein		lycoprotein	E2 glycoprotein precu	ŧπ	hypothetical protein	bacteriocin BCN5 - Cl	98K GTPase-activating	ABR protein 1 - human	ABR protein 2 - human	probable membrane pro		s II beta	SII	uvomoruin - mouse
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predicted #length 999 #molecular-weight 107502 #checksum 8311	SUMMARY
g_site carbohydrate (Asn)	110,180,545
desmoglein repeat #label	937-966
desmoglein repeat #label DG1\	910-938
intracellular #status predicted #label	640-999
transmembrane #status predicted	616-639
cadherin repeat homology #label	496-598
cadherin repeat homology #label	390-495
cadherin repeat homology #label	270-383
cadherin repeat homology #label	160-267
cadherin repeat homology #label	52-157
#domain extracellular #status predicted #label EXT\	50-615
#product desmoglein homolog #status predicted #label	50-999
#domain propeptide #status predicted #label PRO\	24-49
<pre>#domain signal sequence #status predicted #label SIG\</pre>	1-23
,	FEATURE
in	
adhesion;	KEYWORDS
<pre>#superfamily cadherin; cadherin</pre>	CLASSIFICATION
18q12.1-18q12.2	#map_position
##cross-references GDB:134030; OMIM:169615	##Cross-
GDB: DSG3	#gene
	GENETICS
ferences GB:M76482;	##CIOSS-
	##residues
Le_type mRNA	##molecule_
A41088	#accession
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	* 0.1.0.1.0
a novel enithelial cadherin	# + 4 + 1 0
Amagal, M.; Klaus-Kovtun, V.; Stanley, J.K.	#40urnors
	REFERENCE
A41088	ACCESSIONS
	1
30-Jun-1993 #sequence revision 30-Jun-1993 #text change	DATE
pemphigus vulgaris antigen	ALTERNATE_NAMES
	TITLE
IJHUG3 #type complete	ENTRY .
	RESULT 1

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#gene
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of desmoglein gene.

#cross-references_MUID:92037656
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##cross-references GB:S64268; GB:S64270
ENCE A37785
                                                                                                     ##molecule_type mRNA
##residues 44-B001, AQPPSAT' ##label KO3
##cross-references GB:x57784
this sequence has been revised
$38721
                                                                                                                                                                                                                                                                                                                                                                                               ##residues 44-1043 ##label ZIM ##cross-references EMBL:X57784; NID:g436061; PID:g436062
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##cross-references EMBL:X58466; NID:g306; PID:g307
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Biochem. Biophys. Res. Commun. (1990) 173:1224-1230
Desmoglein shows extensive homology to the cadherin
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submitted to the EMBL Data Library, March 1991
Complete sequence of the desmoglein precursor and
for the existence of different desmoglein genes
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#superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
transmembrane protein
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Eur. J. Cell Biol.
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$14603
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                                                                                                                                                                                                                                                                                             Identification of desmoglein, a constitutive desmosomal
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(1990) 53:1-12
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NOE A39706
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Local Similarity 80.0%;
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desmosomal glycoprotein I
formal_name Homo sapiens #common_name man
30-Jun-1993 *sequence_revision 30-Jun-1993
Wheeler, G.N.; Buxton, R.S.; Parker, A.E
Rees, D.A.; King, I.A.; Magee, A.I.
Biochem. Soc. Trans. (1991) 19:1060-1064
Desmosomal glycoproteins I, II and III:
                                                                                                                                                                                          Wagner, R.M.; Green, K.J.
J. Cell Sci. (1991) 99:809-821
Structural analysis and expression
                                                                                                                                                                                                                                                      Nilles, L.A.; Parry, D.A.D.; Powers, E.E.; Angst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wheeler, G.N.; Parker, A.E.; Thomas, C.L.; Ataliotis, Poynter, D.; Arnemann, J.; Rutman, A.J.; Pidsley, S. Watt, F.M.; Rees, D.A.; Buxton, R.S.; Maggee, A.T.; Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800
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Lenox, A.I.; Graham, D.E.; Overbeek, R.; Sr
Keller, M.; Aujay, M.; Huber, R.; Feldman,
J.M.; Olson, G.J.; Swanson, R.V.
Nature (1998) 392:353-358
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                               *superfamily phosphoribosylformylglycinamidine cyclo-ligase, phosphoribosylformylglycinamidine cyclo-ligase homology
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Aquifex aeolicus
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#domain phosphoribosylformylglycinamidine cyclo-ligase
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#cross-references MUID:90232743
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##residues
1-1363 ##label ABR
##coss-references GB:#31053; NID:g323361;
##COTION #superfamily coronavirus E2 glyc
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##molecule_type DNA
##residues 1-441 ##label ROU
##cross-references EMBL:AC003000;
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Deduced sequence of the bovine coronavirus spike protein and identification of the internal proteolytic cleavage site.
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#domain signal sequence #status predicted #label SIG\
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#journal Virology (1991) 183:397-404
#title Comparison of the nucleotide and deduced amino acid sequences
#title of the S genes specified by virulent and avirulent strains
f bovine coronaviruses.
#cross-references MUID:91272503
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##cross-references GB:M64667; NID:g323355; PID:g323356
##ICATION #superfamily coronavirus E2 glycoprotein
DS glycoprotein; transmembrane protein
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submitted to the EMBL Data Library, April 1994
Sequence and functional analysis of the surface protein of
two human Coronavirus OC43 isolates adapted to growth in
MDCK I and Vero cells.
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#product E2 glycoprotein #status predicted #label E2G
#product 90B glycoprotein #status predicted #label EG
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739,788,895,937,
1194,1224,1234,
1253,1267;1288
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18-1363
18-768
769-1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Parker, M.D.; Yoo, D.; Cox, G.J.; Babiuk, L.A.
#journal J. Gen. Virol. (1990) 71:263-270
#title Primary structure of the S peplomer gene of bovine
coronavirus and surface expression in insect cells.
#cross-references MUID:90171910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
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1253,1267,1288
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##residues 1-1363 ##label PAR
##ross references GB:D00662
in the authors' translation residues 23-31 are shown
in the authors' and consequently, residues 32-34 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type genomic RNA
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KITYRISGVGI 14
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Similarity 45.5%;
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90A glycoprotein; 90B glycoprotein
#formal_name bovine coronavirus
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predicted
#length 1363 #molecular-weight 150868 #checksum 6831
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07-Oct-1994
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E2 glycoprotein precursor -
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                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label SIG\
#product E2 glycoprotein #status predicted #label E9B\
#product 90B glycoprotein #status predicted #label E9B\
#product 90A glycoprotein #status predicted #label E9A\
#domain transmembrane #status predicted #label TMN\
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Pred. No.
5; Misma
                                                                         Pred.
                                                                                                             Score 57;
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Best Local
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                                                                                                                                                            #authors Zhang, X.; Kousoulas, K.G.; Storz, J.

*journal Virology (1991) 183:397-404

*title Comparison of the nucleotide and deduced amino acid sequences
of the S genes specified by virulent and avirulent strains

f cross-references MUID:91272503
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714,739,788,895,
937,1194,1224,1234,
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18-768
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#cross-references MUID:90171938
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##residues 1-1363 ##label BOI
##cross-references GB:D00731; NID:g221136; PID:d1001089; PID:g221137
##CATION #superfamily coronavirus E2 glycoprotein
                                                                                               ##molecule_type genomic RNA
##residues 1-1363 ##label ZHA
                                                        ##cross-references GB:M64668
#superfamily coronavirus E2
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90A glycoprotein; 90B glycoprotein
#formal_name bovine coronavirus
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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E2 glycoprotein precursor - bovine coronavirus (strain
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J. Gen. Virol. (1990) 71:487-492
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#product 90B glycoprotein #status predicted #label E9B\
#product 90A glycoprotein #status predicted #label E9A\
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#domain

signal sequence

#status

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CLASSIFICATION

coronavirus

E2

glycoprotein

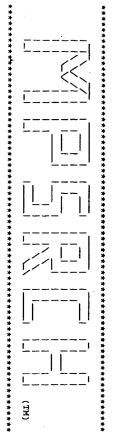
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444,649,676,696,
714,739,788,895,
937,1194,1224,1234,
                                                               #title Comparison of the nucleotide and deduced amino acid sequences of the S genes specified by virulent and avirulent strains of bovine coronaviruses.

#cross-references_MUID:91272503
                                                    #accession
                                                                                                                                                            #authors
                                                                                                                                             #journal
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##cross-references EMBL:233768; NID:9475891; PID:9475892
##CICATION #superfamily coronavirus E2 9lycoprotein
RY #length 1363 #molecular-weight 150701 #checl
             ##molecule_type_genomic RNA
##residues 1-1363 ##label ZHA
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##cross-references GB:M64669
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Similarity 45.5%;
5; Conservative
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Similarity 45.58;
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submitted to the EMBL Data Library, April 1994
Sequence and functional analysis of the surface protein
two human Coronavirus OC43 isolates adapted to growth
MDCK I and Vero cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $44240 #type complete
surface protein - human coronavirus
#formal_name human coronavirus
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
08-Sep-1997
                                                                                                                                       Zhang, X.; Kousoulas, K.G.;
Virology (1991) 183:397-404
                                                                                                                                                                                                 C403
                                                                                                                                                                                                                                                                    peplomer glycoprotein; S glycoprotein;
90A glycoprotein; 90B glycoprotein
                                                                                                                                                                                                                                                                                                       VGIHLY #type complete
E2 glycoprotein precursor -
LY-138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S44240
                                                                                                                                                                                A40320
                                                                                                                                                                                                                              30-Jun-1992 #sequence_revision
                                                                                                                                                                                                                                                   #formal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary
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#product 90B glycoprotein #status predicted #label EGB\
#product 90A glycoprotein #status predicted #label EGA\
                                                                                                                                                                                                                                                 _name bovine coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 2; L
Pred. No. 3.07e+00;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 1; 1
Pred. No. 3.07e+00
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                                                                                                                                                            Storz,
                                                                                                                                                                                                                                                                                                                        bovine coronavirus (strain
                                                                                                                                                                                                                                  30-Jun-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1363;
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                                                                                                                                                                                                                                                                                    glycoprotein
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#authors
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ENTRY
TITLE
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                                                              ALTERNATE_NAMES
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.4%;
Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "journal
#title
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#cross-references MUID:98065943
#accession D70163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      995 NVQYRINGIGV 1005
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4 KITYRISGYGI 14
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                                                                                                                                                                                                                                                                                                                                                                                                                     278 RNIAYRINNINVD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *#@xperimental_source strain B31
(Y ...#length 419 #molecul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 56.4%; Local Similarity 45.5%;
                                                                                                                                                                                                                                                                                                                                               3 QKITYRISGVGID
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                                                                             hypothetical 11.6K protein - strawberry mild yellow edge-associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Hor K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C. Nature (1997) 390:580-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Mile, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Galland, S.; Fujil, C.; Cotton, M.D.; Horst, Vugt, R.V.; Calland, S.; Fujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Fujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Fujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Fujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Horst, V.; Palmer, N. S.; Pujil, C.; Cotton, M.D.; Palmer, N. S.; Palmer, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D70163 #type complete
hypothetical protein BB0509 - Lyme disease spirochete
#formal_name Borrelia burgdorferi #common_name Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 1363
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formal_name strawberry mild yellow edge-associated virus
30-Jun-1992 *sequence_revision 30-Jun-1992 *text_change
31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence not shown;
translation not shown
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#product E2 glycoprotein #status predicted #label EGB\
#product 90B glycoprotein #status predicted #label EGB\
#product 90A glycoprotein #status predicted #label EGA\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #molecular-weight 48741 #checksum
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Pred. No. 3.07e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 2; I
Pred. No. 4.74e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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KEYWORDS
SUMMARY
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REFERENCE
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                                                                                             Query Match 54.5%;
Best Local Similarity 58.3%;
                                                                              Matches
                                                                                                                                                                                                                                                                                                #authors Jelkmann, W.; Maiss, E.; Martin, R.R.
J. Gen. Virol. (1992) 73:475-479
#title The nucleotide sequence and genome organization of strawberry
mild yellow edge-associated potexvirus.
#cross-references MUID:92166762
                                                                                                                                                                                       PID:g222634 PID:g222634
                                                                                                                                                                                                                    ##molecule_type genomic RNA
#*residues 1-108 ##label JEL
##cross-references GB:D12517; DDBJ:D01227; NID:g222631; PID:d1002574;
9 HSITYRILAVGL 20
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3 QKITYRISGVGI 14
                                                                                                                                                    #length 108
                                                                                                                                                                      transmembrane protein
                                                                              Conservative
                                                                                                                                                   #molecular-weight 11589
                                                                        Score 55; DB 2;
Pred. No. 7.28e+
3; Mismatches
                                                                                               55; DB 2; 1
No. 7.28e+00
                                                                                                              Length 108
                                                                            Indels
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                                                                              0
                                                                                                                                                    628
                                                                            Gaps:
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Search completed: Fri Jun 11 17:13:37 1999 Job time: 84 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated Run on: Fri Jun 11 17:09:17 1999; MasPar time 2.55 Seconds 166.490 Million cell updates/sec

Description: Perfect Score: >US-08-991-628-1 (1-15) from US08991628.pep 101 1 ATOKITYRISGVGID 15

Title:

Scoring table: PAM 150 Gap 15

Searched: 77977 segs, 28268293 residues

Post-processing: Minimum Match Listing first 0% 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 26.539; Variance 30.462; scale 0.871

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P P P P I			DB DB
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DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3.

SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.

	45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	2.4
	51	51	51	51	51	51	51	51	51	51	51	51	51	52	52	52	52	52	52	53	53	53
	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	51.5	51.5	\mathbf{L}	51.5	51.5	51.5	52.5	52.5	52.5
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	P2P_LACPA	CHD1_MOUSE	CHD1_HUMAN	BCR_HUMAN	YK83_YEAST	CAD4_HUMAN	CAD4_MOUSE	CAD1_CHICK	IMDH_BACSU	MYOC_HUMAN	IMDH_STRPY	YB57_YEAST	S3AC_BACSU	VGL2_CVMA5	DYNA_DROME	YJ09_YEAST	TSP3_MOUSE	HFE1_HAEIN	TONB_KLEPN	VGL2_CVM4	VGL2_CVMJC	PUR2_CHITE
•	PII-TYPE PROTEINASE PR	CHROMODOMAIN-HELICASE-	CHROMODOMAIN-HELICASE-	BREAKPOINT CLUSTER REG	PROBABLE ATP-DEPENDENT	RETINAL-CADHERIN PRECU	RETINAL-CADHERIN PRECU	EPITHELIAL-CADHERIN PR	INOSINE-5'-MONOPHOSPHA	MYOCILIN PRECURSOR (TR	INOSINE-5'-MONOPHOSPHA	HYPOTHETICAL 51.5 KD P	STAGE III SPORULATION	E2 GLYCOPROTEIN PRECUR	150 KD DYNEIN-ASSOCIAT	HYPOTHETICAL 127.4 KD	THROMBOSPONDIN 3 PRECU	MINOR FIMBRIAL SUBUNIT	TONB PROTEIN.	E2 GLYCOPROTEIN PRECUR	E2 GLYCOPROTEIN PRECUR	PHOSPHORIBOSYLAMINE G
	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	1.30e+01	8.19e+00	8.19e+00	8.19e+00	8.19e+00	8.19e+00	8.19e+00	5.14e+00	5.14e+00	5.14e+00

ALIGNMENTS

<u>:</u>	RL CELL 67:869 CC -!- FUNCTIC CC INVOLVE CC FILAMEN CC -!- SUBCELL		DSG3. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; C PRIMATES; CATARRHINI;	P32926; 01-OCT-1993 01-OCT-1993 01-NOV-1997 DESMOGLEIN	RESULT 1 ID DSG3_HUMAN
TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS CARCINOMAS. DOMAIN: CALCTUM MAY BE BOUND BY THE CADHERTN-LIKE REPEATS	CELL 67:869-877(1991). -I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS FILAMENTS MEDIATING CELL-CELL ADHESIONI- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	[1] SEQUENCE FROM N.A. MEDLINE; 92069753. MEDLINE; 92069753. "AMAGAI M., KLAUS-KOYTUN V., STANLEY J.R.; "Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion.";	DSG3. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.	P32926; 01-OCT-1993 (REL. 27, CREATED) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DESMOGLEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA).	STANDARD;
MIS, TONGU	ERCELLULAI N OF PLAQU ELL ADHES: I MEMBRAN	ANLEY J.R l epithel: lhesion.";	VERTEBRATI E; HOMO.	DEMPHIGUS	PRT; 999
JE, TONSIL,		; lal cadherin	\; MAMMALIA;	ATE) DATE) VULGARIS A	999 AA.
OESOPHAGUS AND	JUNCTIONS. AND INTERMEDIATE	ı in pemphigus	EUTHERIA;	NTIGEN) (PVA).	

EMBL; M76482; G190752; -.
PIR; A41088; IJHUG3.
MIN; 169615; -.
PROSITE: PS00232; CADHERIN; 3
PFAM; PF00028; cadherin; 4.
HSSP; P09803; 1EDH. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). ω

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SEQUENCE OF 44-455 .....

SEQUENCE OF 44-455 .....

MEDLINE; 91097553.

X "Desmoglein shows extensive homology to the cadherin fa adhesion molecules ";

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SIGNAL 1
PROPEP 24
CHAIN 50
                                                                                                                                                                                                            MEDLINE; 920:
KOCH P.J., GO
FRANKE W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
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"Identification of desmogle:
glycoprotein, as a member oo
molecules.";
EUR. J. CELL BIOL. 53:1-12(
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MEDLINE; 91168965.
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CARBOHYD
                                                                                                                                                                   "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene."; {\tt SUR}. J. CELL BIOL. {\tt 55:200-208(1991)}.
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BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDA
ARTIODACTYLA; RUMINANTIA;
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01-NOV-1997
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Q03763;
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DISSUE-MUZZLE EPITHELIUM;
GOLDSCHMIDT M.
GOLDSCHMIDT M.
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Similarity 100.0%;
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3 (REL. 27, L.
7 (REL. 35, L.
1 PRECURSOR
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ANTIA; PECORA; BOVOIDEA; BOVIDAE;
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R (DESMOSOMAL GLYCOPROTEIN I)
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DBJ DATA BANKS.
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Matches
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TISSUE-KERATINOCYTES;
MEDLINE; 91271279_.
WHEELER G.N., PARKER A.E.,
ARNEMANN J., RUTMAN A.J., E
BUXTON R.S., MAGEE A.I.;
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DESMOGLEIN 1 PRECURSOR
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EMBL; X57784; G436062; -.
EMBL; M58165; G552318; -.
PIR; S14603; LJBOG1.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as not removed. modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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HSSP; P09803; 1EDH.
CELL ADHESION; SIGNAL; TI
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                                                              EQUENCE FROM N.A.
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TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND OESOPHAGUS
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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SIMILARITY:
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                                                                                      CATARRHINI;
                                                                                                  WETAZOA; CHORDATA;
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larity 80.0%;
Conservative
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                                                                                      HOMINIDAE;
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              , THOMAS
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              WATT F.M.,
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VIGNA UNGUICULATA (COWPEA).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYGEUKARYOTA; WAGNOLIOPHYTA; EMBRYGEUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA.
                                                                                              PURS_VIGUN STANDARD; PRT; 388 AA.

P52424;

01-OCT-1996 (REL. 34, CREATED)

01-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)

01-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)

PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LICASE PRECURSOR (EC 6.3.3.1)

CAIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE).
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PROPEP
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PROC. NATL. ACAD. SCI. U.S.A. 88:4796-4800(1991).

-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDI FILAMENTS MEDIATING CELL-CELL ADHESION.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE TONGUE, TONSILAND OESOPHAGUS.

-!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND OESOPHAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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REPEAT
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SIMILARITY: BELONGS
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Pred. No.
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DESMOGLEIN REPEAT 1

DESMOGLEIN REPEAT 2

DESMOGLEIN REPEAT 2

DESMOGLEIN REPEAT 4
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EXTRACELLULAR (
POTENTIAL.
CYTOPLASMIC (PC
CADHERIN 1.
CADHERIN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1; L, 3.06e-08;
                                        EMBRYOPHYTA;
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AND INTERMEDIATE
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Best Local Similarity
Matches 9; Conse
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                                                                                                                                                             ABRAHAM S., KIENZLE T.E., LAPPS W.E., BRIAN D.A.;
"Sequence and expression analysis of potential nor
of 4.9, 4.8, 12.7, and 9.5 kDa encoded between the
protein genes of the bovine coronavirus.";
VIROLOGY 177:488-495(1990).

-i- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE B:
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YUL2_CVBM STANDARD; PRT; 1363 AA.
P15777;
01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. VITA 3; TISSUE-ROOT NODULES;
SMITH P.M.C., MANN A.J., HALL D.J., ATKINS C.A.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CAPALYTIC ACTIVITY: ATP + 5'-PHOSPHORIBOSYL-FORMYLGLYCINAMIDINE
ADP + ORTHOPHOSPHATE + 5'-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE.
-!- PATHWAY: FIFTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 90232743.
ABRAHAM S., KIENZLE T.E., LAPPS W.E., BRIAN D.A.;
"Deduced sequence of the bovine coronavirus spike protein identification of the internal proteolytic cleavage site."
VIROLOGY 176:296-301(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOVINE CORONAVIRUS (STRAIN MEBUS).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
CORONAVIRIDAE; CORONAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SEQUENCE FROM N.A.
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|:|:||:||:|| 11
1 ATQKITYRISGVGID 15
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SIMILARITY: TO OTHER AIRS FROM BACTERIA AND EUKARYOTES.
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PHOSPHORIBOSYLFORMYLGLYCINAMIDINE
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5.81e-02;
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Matches
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                                                                                               SEQUENCE FROM N.A.

MELLINE; 91272503.

ZHANG X., KOUSOULAS K.G., STORZ J.;

"Comparison of the nucleotide and deduced amino acid sequences of t
"Comparison of the nucleotide and avirulent strains of boyine
s genes specified by virulent and avirulent strains of boyine
coronaviruses."

VIROLOGY 183:397-404(1991).

"ITO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
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SEQUENCE
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EMBL; M64669; G323360; -. PIR; C40320; VGIHLY.
                                                                                                                                                                                                          VIRUSES;
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                                                                                                                                                                                                CORONAVIRIDAE;
                                                                                                                                                                                                                 BOVINE CORONAVIRUS
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P25192;
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les 5; Conse
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; M31054; G323364;
A34607; VGIHNM.
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POSITIVE-STRAND VIRUSES,
                                                                                                                                                                                                                                                                                    STANDARD;
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1194
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45.5%;
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17 POTENTIAL.
363 SPIKE E2 GI
SPIKE PROJ
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Pred. No. 7.46e-01;
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CYTOPLASMIC
CYS-RICH.
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SPIKE PROTEIN S2 (90A).
EXTRACELLULAR (POTENTIAL).
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Best Local S
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      GLYCOPROTEIN;
SIGNAL
CHAIN
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01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE; 90171910.

PARKER M.D., YOO D., COX G.J., BABIUK L.A.;

SUIFACE SETUPLIANCE OF LOWER PROTEIN MEDIATES THE BINDING OF VIRIONS

TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGL2_CVBQ
P25193;
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CARBOHYD
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CARBOHYD
                                                                                       PIR;
                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOVINE CORONAVIRUS (STRAIN QUEBEC).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
CORONAVIRIDAE; CORONAVIRUS.
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN)
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                                                                                                      D00662; G221139;
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Similarity 45.5%;
5; Conservative
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PROTEIN, TRANSMEMBRANE; SIGNAL.
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SPIKE E2 GLYCOPROTEIN.
SPIKE PROTEIN S1 (90B).
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Pred. No. 7.46e-01;
5; Mismatches 1
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SPIKE PROTEIN S1 (90B).
SPIKE PROTEIN S2 (90A).
EXTRACELLULAR (POTENTIAL)
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W; 006A5E61 CRC32;
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PZ5194;
01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN)
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                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           VIROLOGY 183:397-404(1991).
-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                                                                                                                                                                                                                                                                             "Comparison of the nucleotide
S genes specified by virulent
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ZHANG X., KOUSOULAS K.G.,
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VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
CORONAVIRIDAE; CORONAVIRUS.
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similarity 45.5%;
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SPIKE E2 CLYCOPROTEIN.

SPIKE PROTEIN S1 (90B).

SPIKE PROTEIN S2 (90A).

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R (POTENTIAL).
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BOIREAU P., CRUCIERE C., LAPORTE J.;
"Nucleotide sequence of the glycoprotein S gene coronavirus and comparison with the S proteins o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVINE CORONAVIRUS (STRAIN F15)
VIRUSES; SSRNA POSITIVE-STRAND
CORONAVIRIDAE; CORONAVIRUS.
                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (see http://www.isb-slb.or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsi
                                                                                                                                                                                                                                                                                                                           VITUS STRAINS.";
J. GEN. VIROL. "1:487-492(1990).
-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
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GLYCOPROTEIN;
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SPIKE E2 GLYCOPROTEIN.

SPIKE PROTEIN S1 (90B).

SPIKE PROTEIN S2 (90A).

EXTRACELLULAR (POTENTIAL,

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CYTOPLASMIC (POTENTIAL).

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POTENTIAL.
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Pred. No. 7.46e-01;
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Best Local Similarity
Matches 5; Conser
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MEDLINE; 91272593.

ZHANG X., KOUSOULAS K.G., STORZ J.;

ZHANG X., KOUSOULAS K.G., STORZ J.;

"Comparison of the nucleotide and deduced amino acid sequences of t

"Comparison of the nucleotide and avirulent strains of bovine

S genes specified by virulent and avirulent strains of bovine

coronaviruses.";

VIROLOGY 183:397-404(1991).

-i- FUNCTION: THE PEPELOMER PROTEIN MEDIATES THE BINDING OF VIRIONS

-i- FUNCTION: THE PEPELOMER PROTEIN MEDIATES THE BINDING OF VIRIONS

TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
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P25191;
01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).
                                                                                                                                                             EMBL; M64667; G323356; -. PIR; A40320; VGIHL9.
                                                                                                                                                                                                                                                                                                                                                                                                                             BOVINE CORONAVIRUS (STRAIN L9).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES,
                                                                                                              CHAIN
                                                                                                                          CHAIN
                                                                                                                                                  GLYCOPROTEIN;
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                                                                      SPIKE E2 GLYCOPROTEIN.
SPIKE PROTEIN S1 (90B).
SPIKE PROTEIN S2 (90A).
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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Pred. No. 7.46e-01;
5; Mismatches 1
CYTOPLASMIC
CYS-RICH.
POTENTIAL.
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POTENTIAL.
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                                                                                                                                               TRANSMEMBRANE; SIGNAL
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                                                            (POTENTIAL)
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P75118;
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JELKMANN W., MAISS E., MARTIN R.R.;
JELKMANN W., MAISS E., MARTIN R.R.;
JELKMANN W., MAISS E., MARTIN R.R.;

"The nucleotide sequence and genome organization of strawberry mil
yellow edge-associated potexvirus.";

J. GEN. VIROL. 73:475-479(1992)

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-!- SIMILARITY: TO ORF3 PROTEIN FROM OTHER POTEXVIRUSES AND TO 12
PROTEIN FROM CARLAVIRUSES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 35, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL 30, LAST ANNOTATION UPDATE)
11.5 KD MEMBRANE PROTEIN (ORF 3).
STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEAV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTEXVIRUS.
                                                                                                                                                                                     EMBL; D12517; G222634; -. PIR; JQ1428. JQ1428. PFAM; PF01307; Plant_vir_prot;
                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-MY-18
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                    9 HSITYRILAVGL 20
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108 AA;
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                                                                                                Score 55; DB 1; 1
Pred. No. 1.99e+00;
3; Mismatches 1
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Pred. No. 7.46e-01;
5; Mismatches 1
                                                                                                                                             POTENTIAL.
POTENTIAL.
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W; 54233485 CRC32;
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Best Local S
Matches
                                                                                                                                                                                                  DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.

AP50 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR (POTENTIAL).

-I- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 2 (AP-2) IS AN HETEROTETRANBER COMPOSED OF TWO LARGE CHAINS (ALPHA AND BETA), A MEDIUM CHAIN (AP50) AND A SMALL CHAIN (AP17) (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE CYTOPLASMIC FACE OF COATED VESICLES IN THE PLASMA MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PUTATIVE CLATHRIN COAT ASSEMBLY PROTEIN AP50 (CLATHRIN COAT ASSOCIATED PROTEIN AP50) (PLASMA MEMBRANE ADAPTOR AP-2 50 KD PROTEIN) (HA2 50 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 MEDIUM CHAIN).
SPAC31A2.09C.
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STRAIN-ATCC 29342 / M129;
MEDLINE; 97105885.
HIMMELÆEICH R., HILBERT H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYCOPLASMA PNEUMONIAE.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOY-1997 (REL. 35, CREATED)
01-NOY-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOY-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN MG459 HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
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Q09718;
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Similarity 46.7%;
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Pred. No. 1.99e+00,
4; Mismatches '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLAGENS
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                                                                                                                                                               ADAPTOR COMPLEXES
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -

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Matches
                                     Query Match 54.5%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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01-MAR-1992
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                               HYDROLASE;
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    beta-galactosidase gene cloned in Escherichia coli.";

J. BACTERIOL. 173:3084-3095(1991).

-i- CAPALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

-i- INDUCTION: LATE IN THE ABE (ACETONE, BUTANOL, AND ETHANOL)
FERMENTATION AND SUBJECT TO GLUCOSE REPRESSION.

-i- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z50113; G914887; -.

PROSITE; PS00990; CLAT_ADAPTOR_M_1; 1.

PROSITE; PS00991; CLAT_ADAPTOR_M_2; 1.

PFAM; PF00928; Adap_comp_sub; 1.

HYPOTHETICAL PROTEIN; COATED PITS.

SEQUENCE 446 AA; 50821 MW; C97D83CC
                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBGA.
                                                                                                                                                                     PFAM;
                                                                                                                                                                                 EMBL; M35107; G144746; -.
PIR; A39405; A39405.
PROSITE: PS00719; GLYCOSYL_HYDROL_F2_1;
PROSITE: PS00608; GLYCOSYL_HYDROL_F2_2;
                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCOTT D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 91216979.
HANCOCK K.R., ROCKMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-NCIB 2951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLOSTRIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLOSTRIDIUM ACETOBUTYI BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA-GALACTOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BGAL_CLOAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Expression and nucleotide sequence
828 KITYEVSGEGI 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 SKQKIIYRIS
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                                                                                                                                                        PF00703;
P00722; 1
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                                                                                             459
503
897
                                                                                                                           GLYCOSIDASE.
459 459
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(REL. 33, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNOTATION UPDATE)
OSIDASE (EC 3.2.1.23) (LACTASE).
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                                                                                                                                                        ; glycosyl_hydro7;
lBGL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOUNG C.A., PEARCE L., MADDOX I.S.,
                                                                                                MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 1; 1
Pred. No. 1.99e+00;
1; Mismatches 3
                                      Score 55; DB 1; L
Pred. No. 1.99e+00;
1; Mismatches 2
                                                                                             PROTON DONOR (BY SIMILARITY)
NUCLEOPHILE (BY SIMILARITY).
N; 5CFF268B CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the Clostridium
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                                                                    Length
                                           Indels
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4 KITYRISGVGI 14

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RESULT 15
ID CRU1_RAPSA STANL...
AC Q02498;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DT CRUCIFERIN PGCRURSE5 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN).

""PEPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; ROSII
                                                                               ş
                                                                                                                       В
Search completed: Fri Jun 11 17:09:28 1999 Job time: 11 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.5%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                           DISULFID
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CV. SAAK KNACKER;
MEDLINE; 93043037.

DEPIGNY-THIS D., RAYNAL M., ASPART L., DELSENY M., GRELLET F.;
"The cruciferin gene family in radish.";
PLANT MOL. BIOL. 20:467-479(1992),
-1- FUNCTION: THIS IS A SEED STORAGE PROTEIN.
-1- SUBUNIT: HEXAMER; EACH SUBUNIT IS COMPOSED OF AN ACIDIC AND A BASIC CHAIN DERIVED FROM A SINGLE PRECURSOR AND LINKED BY A DISULFIDE BOND.
-1- SIMILARITY: BELONGS TO THE 11S SEED STORAGE PROTEINS (GLOBULINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRUKS., RADISH).

RAPHANUS SATIVUS (RADISH).

EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE; CAPPARALES; BRASSICACEAE; RAPHANUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X59808; G21118; -.
                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S26223; S26223.
PROSITE; PS00305; 11S_SEED_STORAGE; 1.
                                                                                                                   92 SSPKIAYVVQGMGI 105
                                                                             :: ||:| : |:||
1 ATQKITYRISGVGI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY.
                                                                                                                                                                                                                                                                                                       PF00190; Seedstore_11s; 1.

STORAGE PROTEIN; SIGNAL; MILTIGENE FAMILY.

1 23 BY SIMILARITY.

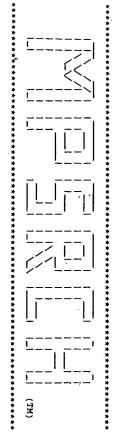
BY SIMILARITY.

BY SIMILARITY.

CRUCIFERIN PGCRURSE

CRUCIFERIN PGCRURSE

FID 113 296 INTERCHAIN (ALPHA-B)
                                                                                                                                                                                                                                           211
479 AA;
                                                                                                                                                                                                                                         218 P
53256 MW;
                                                                                                                                                     Score 54; DB 1; Length 479; Pred. No. 3.21e+00; 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                               BY SIMILARITY.
CRUCIFERIN PGCRURSES ALPHA CHAIN.
CRUCIFERIN PGCRURSES BETA CHAIN.
INTERCHAIN (ALPHA-BETA) (POTENTIAL).
CLN/GLY-RICH.
                                                                                                                                                                                                                                                                POLY-GLN
                                                                                                                                                                                                                                         2A5DEA90 CRC32;
                                                                                                                                                       0;
                                                                                                                                                       Gaps
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Jun 11 17:09:46 1999; MasPar time 6.16 Seconds 132.927 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-991-628-1 (1-15) from US08991628.pep

ATQKITYRISGVGID 15

Scoring table:

PAM 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 25.479; Variance 31.590; scale 0.807

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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52.5	52.5	52.5	52.5	52.5	52.5	53.5	53.5	53.5	53.5	54.5	55.4	56.4	•	56.4	•	58.4	59.4	91.1	Query Match
780 780	280	82	82	82	82	2610	878	482	287	108	419	1363	1363	441	331	2269	3380	993	Length
22	ω	7	7	7	7	ű	4	N	u	14	N	14	14	10	N	ر.	v	11	ВВ
068332 P77846	005871	Q31538	Q31537	Q31536	077862	Q19482	Q15855	059326	Q20481	041278	051462	Q66290	Q66291	022282	066968	077360	024292	035902	Ħ
HYPOTHETICAL 43.9 KD P CELLODEXTRIN-PHOSPHORY	E XII COS	II BETA		MHC CLASS II BETA CHAI	MHC CLASS II B LOCUS 4	F15B9.7 PROTEIN.	UVOMORULIN PRECURSOR (CHITINASE PRECURSOR (E	F46G10.3 PROTEIN.	STRAWBERRY MILD YELLOW	HYPOTHETICAL 48.7 KD P	SURFACE PROTEIN PRECUR	SURFACE PROTEIN PRECUR	T517.1 PROTEIN.	PHOSPHORIBOSYLFORMYLGL	MAL3P4.25 PROTEIN.	ADHERIN.		Description
1.06e+01 1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	6.74e+00	6.74e+00	6.74e+00	6.74e+00	4.25e+00	2.67e+00	1.66e+00	1.66e+00	1.66e+00	1.03e+00	6.36e-01	3.90e-01	8.44e-09	Pred. No.

45	44	43	42	41	40	39	3 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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S GLYCOPROTEIN.	SPIKE PROTEIN.	SPIKE GLYCOPROTEIN.	E2 GLYCOPROTEIN PRECUR	F02E9.6 PROTEIN.	XMN-CADHERIN (FRAGMENT	F56H6.7 PROTEIN.	ABCA (FRAGMENT).	PHOSPHOGLUCOMUTASE A.	12S CRUCIFERIN SEED ST	CAP8E.	CAPSE.	HYPOTHETICAL 36.1 KD P	_	HYDROXYMETHYLGLUTARYL-	F35G12.10 PROTEIN.	P2604 PROTEIN (ORF YPL	12S STORAGE PROTEIN (F	S GLYCOPROTEIN.	SURFACE GLYCOPROTEIN S	SURFACE PROTEIN.	PDR5-LIKE ABC TRANSPOR	HYPOTHETICAL 108.0 KD	GUANINE NUCLEOTIDE REG	ABR.
1.66e+01	1.66e+01	1.66e+01	1.66e+01		1.66e+01	٠	1.66e+01			1.66e+01				1.66e+01	•	1.66e+01		1.06e+01	1.06e+01	1.06e+01		1.06e+01	1.06e+01	1.06e+01

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OI-NOV-1998 (TREMBLEEL 08, LAST ANNOTATION UPDATE) OI-NOV-1998 (TREMBLEEL 08, LAST ANNOTATION UPDATE) ADHERIN. DACHSOUS. DROSOPHILA MELANOGASTER (FRUIT FLY). EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA; PTERYGOTA; DIPPERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;	PRELIMINARY; PRT; 3380 i	Query Match 91.1%; Score 92; DB 11; Length 993; Best Local Similarity 100.0%; Pred. No. 8.44e-09; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 81 QKITYRISGYGID 93	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-BALB/C; STRAIN-BALB/C; ISHIKAWA H., LI K., UITTO J.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. -!- SUDERLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY). EMBL; U86016; G2290200; PROSITE; PS00232; CADHERIN; 2. PFAM; PF00028; CADHERIN; 2. PFAM; PF00028; cadherin; 4. CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT. NON_TER 993 993 SEQUENCE 993 AA; 107888 MW; 881794BD CRC32;	RESULT 1 ID 035902 PRELIMINARY; PRT; 993 AA. AC 035902; PRELIMINARY; PRT; 993 AA. AC 035902; PRELIMINARY; PRT; 993 AA. DT 01-VAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DE DESMOGLEIN 3 (FRAGMENT). DE DESMOGLEIN 3 (FRAGMENT). OS MUS MUSCULUS (MOUSE). OS MUS MUSCULUS (MOUSE). CEUKRAYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.

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RESULT
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FIYBASE; FB9n000497; ds.
PROSITE; PS00232; CADHERIN; 18.
PPAM; PF00028; Cadherin; 26.
CELL ADHESION; GLYCOPROTEIN; TRANS
SEQUENCE 3380 AA; 366356 MW; 7
                                                                               MEDLINE; 98196666.

DECKERT G., WARREN P.V., GA
GRAHAM D.E., OVERBEEK R., S
FELDMAN R.A., SHORT J.M., O
"The complete genome of the
FELDMAN R.A., S
"The complete caeolicus.";
NATURE 392:353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  066968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        077360
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                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMLIN N., LAWSON D., BARRELL B.;
SUBMITTED (OCT-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AL008970; E1332566; -.
SEQUENCE 2269 AA; 267233 MW; 11E1C8E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                        PURM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-3D7;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                        BACTERIA;
                                                                                                                                                                                                                                                                                                                           AQUIFEX AEOLICUS.
BACTERIA; AQUIFICALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAL3P4.25 PROTEIN.
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GENES DEV. 9:1530-1542(1995).
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 8; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KITYRISGVGID
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7; Conse
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ALVEOLATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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88
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                                                                                                                                                                                                                                                                                                                           AQUIFICACEAE;
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                                                                               , GAASTERLAND T., YOUNG W.G.,
SNEAD M.A., KELLER M., AUJ.,
OLSON G.J., SWANSON R.V.;
the hyperthermophilic bacter
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LAST SEQUENCE UP
LAST ANNOTATION 1
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Pred.
0; M
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Pred.
2; M
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MW; 7D83FAC3 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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6.36e-01
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3.90e-01
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                                                                                                                                      AUJAY M.,
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STRAIN-CV. COLUMNATOR OF THE C
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Best Local
Matches
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Best Local S
Matches
                                                                                                                                                                               01-NOV-1996 (TREMBI
01-MAY-1997 (TREMBI
SURFACE PROTEIN PRI
HUMAN CORONAVIRUS.
VIRUSES; SSRNA POSI
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01-JAN-1998 (TREMBLR
01-JUN-1998 (TREMBLR
1517.1 PROTEIN
T517.1 OR F17A14.8.
                                                                                                                                                                                                                                                                                                                                                              Q66291;
Q66291;
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DECKERT G., WARREN P.V., GAASIERT KELLER M., AUG.
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUG.
GRAHAM R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
SEQUENCE FROM N.AT
STRAIN-HCV-CC43;
KUENKEL F., HERKLER G.;
ARCH. VIROL. 1411:1123-1131(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRA
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAM
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYTLOCHYTES; SERENATOPHYTA; MEGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                   VIRUSES; SSRNA
CORONAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N. STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 SGQKLLYRVNGAGSE
: {|: ||::| |:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 58.3%; tes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 40.0%, 6; Conservative
                                                                                                                                                                                                                                      (TREMBLREL. 01, (TREMBLREL. 01, (TREMBLREL. 03, TEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TREMBLREL.)
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                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                POSITIVE-STRAND CORONAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
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58.3%;
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                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE ANNUAL AST ANNUAL AST
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K.A., CROSBY M.L., BRANI
., KERLAVAGE A.R., ADAMS
                                                                                                                                                                         VIRUSES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4C3D13B0 CRC32;
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ANNOTATION
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SURFACE PROTEIN PRECURSOR.
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                                                                                                                                                                                                                      FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A. LATHICRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., C DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D., PETERSON J., KERLAVAGE A.R., OUACKENBUSH J., SALZBERG S., HANS VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J., UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
   burgdorferi.";
NATURE 390:580-586(1997).
EMBL; AE001153; G2688429;
TIGR; BB0509; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-ATCC 35210 / MEDLINE; 98065943.
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ARCH. VIROL. 1411:1123-1131(1996).
EMBL; Z32768; G475892; -.
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VIRUSES; SSRNA POSITIVE-STRAND
CORONAVIRIDAE; CORONAVIRUS.
                                                                                                                                                                   GARLAND S., FUJII C.,
SMITH H.O., VENTER J.
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L MW; 4510BD9B (
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LAST SEQUENCE UPDATE)
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Pred. No.
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SURFACE PROTEIN.
MW; A2808D88 CRC32;
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LAMPRECHT S., JELANDECH.

ACTA HORTICULTURAE 0:0-0(0).

EMBL; Y13938; E324688; -

EMBL; Y13938; E324688; -

PFAM; PF01307; Plant_vir_prot; 1.

PFAM; PF01307; Plant_vir_prot; 1.
elegans.";
NATURE 368:32-38(1994).
EMBL; Z50177; E1346901;
TENTENCE 287 AA; 324(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
01-JAN-1999
F46G10.3 PRO
                                                                                                                                                                                                 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COOLSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMOR B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN :
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATERSON A., WATERSTON R., VAUGHAN K., WATERSTON R.,
WATERSON A., WATERSTON R., WATERSTON R.,
WATERSON A., WATERSTON R., WATERSTON R.,
WATERSTON R., WATERSTON R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
COLES L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q20481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-ONV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLEREL. 08, LAST ANNOTATION UPDATE)
STRAWBERRY MILD YELLOW EDGE-ASSOCIATED POTEXVIRUS COA
PARTIAL REPLICASE AND ORF2, ORF3, ORF4
STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEAV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                            WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 RNIAYRINNINVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OKITYRISGVGID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TREMBLREL.)
(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.4%;
larity 38.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%;
                          32464 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48741 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; D
Pred. No. 2.
6; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
3; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                          F4C7797C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1D982A03 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7389D9CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     re 56; DB 2; L
d. No. 2.67e+00;
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55; DB 14;
No. 4.25e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO DNA STAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTEXVIRUS
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Query Match Best Local

Similarity

DB 5; I 6.74e+00;

Length

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SOLUTION OF COLUMN AND COLUMN AND
RESULT OF STREET OF STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q15855
Q15855; Q16194; Q13799;
Q15855; Q16194; Q13799;
Q1-NOV-1996 (TREMBLREL 01, C
Q1-NOV-1996 (TREMBLREL 01, L
Q1-NOV-1998 (TREMBLREL 08, L
                    SEQUENCE OF 333-472 FROM N.A. MEDLINE; 94306394.
BECKER K.F., ATKINSON M.J.,
SIEWERT J.R., HOFLER H.;
"E-cadherin gene mutations ;
                                                                                                                                                                                                             CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-DSM 1237;
STRAIN-DSM 1237;
FUCHS K.P., SCHWARZ W.H., STAUDENBAUER W.L.;
SUBMITTED (JAN-1996) TO EMBL/GENBAUK/DDBJ DATA BANKS.
SUBMITTED (ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 11
Q59326 ,
Q59326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLOSTRIDIUM THERMOCELLUM. BACTERIA; FIRMICUTES; BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UVOMORULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00404; celCC; 2.
PFAM; PF00704; glycosyl_hydro8; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS010448; CLOS_CELLULOSOME_RPT; PROSITE; PS01095; CHITINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLOSTRIDIUM
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE)
(1.4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL; HYDROLASE; GLYCOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                            ISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
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ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-ACETYL-D-GLUCOSAMINE POLYMERS OF 268924; E220269; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYRFDGVDID 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATMKLDYRISDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.5%;
larity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482
55028 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (E-CADHERIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACILLUS/CLOSTRIDIUM
                                                                                                                                                                                                                           COMMUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54;
Pred. No. |
1; Misma
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Pred. No. 6.
1; Mismatci
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LAST ANNOTATION UPDATE)
HERIN) (ARC-1/UVOMORULIN).
                                                                                         REICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                    200:1754-1761(1994)
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                                                                                  α.,
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                              clues
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                                                                                     BECKER I.,
                                                                                                                                                                                                                                                                                     suggests a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2:
                                                                                         NEKARDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                    type gastric
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RESULT AND SELECTION OF THE SULT AND SELECTI
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Query Match
Best Local Similarity
Matches 7; Conse
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EMBL; S72492; E136801; -...
EMBL; S72491; E136801; JOINED
EMBL; X52279; G28822; -...
PROSITE; PS00232; CADHERIN; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JLT 13
Q1948; PRELIMINARY;
Q1948; Q23218; UP-NOV-1996 (TREMBLREL. (
01-NOV-1998 (TREMBLREL. (
01-NOV-1998 (TREMBLREL. (
01-AUG-1998 (TREMBLREL. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONNFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULS
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON
JONES M., KERSHAW J., KIRSTEN J., LAISTER M., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER B., O'CALLAGHAN
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNK
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
                                                                                                                                                                                                                                                                                                                                                                                                                            elegans
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[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WATSON A., WEINSTOCK L., "2.2 Mb of contiguous nu elecans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F15B9.7 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF01049; Cadherin_C_term; 1.
CELL ADHESION; GLYCOPROTEIN; TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRIXEN U.H.;
SUBMITTED (MAR-1990)
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
PERCY C.;
                                                                                                                                                                                                                                                                                                                                                                                               NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON WATERSTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAYNES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          515 QKITYRI 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54:3845-3852(1994).
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larity 100.0%;
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                                                                                                                                                                                                                                           TO EMBL/GENBANK/DDBJ
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TION: TYPE I MEMBRANE
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07,
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Pred. No.
0; Misma
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LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE;
POTENTIAL.
                   TRANSMEMBRANE; CALCIUM-BINDING; 1D187623 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UVOMORULIN
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. 6.74e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEA; RHABDITIA; RHABDITIDA;
PELODERINAE; CAENORHABDITIS.
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                                                                                                                                                                                                                                     DATA BANKS.
PROTEIN (BY
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PROTEIN (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOHNSTON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COULSON
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RESULT 14

O77862 PRELIMINARY; PRT; 82 AA.

AC 077862 PREMBLREL. 08, CARATED)

OT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

OT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

OT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE MHC CLASS II B LOCUS 4 (FRAGMENT).

OC CLASS II B LOCUS (NILE TILAPIA) (TILAPIA NILOTICA).

EUKARYOTA; METAZOA; CHORDATA; VETTEBRATA; ACTINOPTERYGII; NEOPTERYGII;

OC CLASSOLICE; CICHLIDAE; TILAPIA.

(1)

RP SEQUENCE FROM N.A.

RA MEDLINE; 98315113.

RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,

RA SUBLIVMANN H., FIGUEROA F., KLEIN J.;

RI "Linkage Relationships and Haplotype Polymorphism among Cichlid MHC class II B genes.";

RL GENETICS 149:1527-1547(1998).

DR EMBL; AF049971; G3282889; -.

KW MHC.

FT NON_TER 82

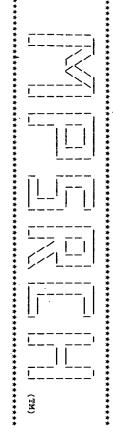
SQ SEQUENCE 82 AA; 9607 MW; D1718622 CRC32;
                                                                          Query Match
Best Local S
Matches
   Query Match 52.5%;
Best Local Similarity 50.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                O31536 PRELIMINARY; PRT; 82 AA.
O31536; CREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MHC CLASS II BETA CHAIN (FRAGMENT).
                                                                                                                                             ONO H., O'HUIGIN C., TICHY H., KLEIN J.;
"Major-histocompatibility-complex variation
fishes from Lake Malawi.";
MOL. BIOL. EVOL. 10:1060-1072(1993).
EMBL; L17460; G309928; -.
EMBL; L17460; G309928; -.
EMBL; PF00969; MHC_II_beta; 1.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 94018589.
ONO H., O'HUIGIN C.,
                                                                                                                                                                                                                                                                                                              PSEUDOTROPHEUS ZEBRA.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; P
LABROIDEI; CICHLIDAE; PSEUDOTROPHEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               612 QKITYRI 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match
Local Similarity 50.0%;
hes 7; Conservative
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82
82 AA;
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9754 MW;
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Pred. No. 6.74e+00;
0; Mismatches 0
   Score 53; DB 7; Len
Pred. No. 1.06e+01;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 7; L
Pred. No. 1.06e+01;
4; Mismatches 3
                                                                          90E5E756 CRC32;
                                                                                                                                                                                                                                                                                                                              ; ACTINOPTERYGII; NEOPTERYGII; PERCOMORPHA; PERCIFORMES;
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••
                                     Length 82;
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                                                                                                                                                                                                                      two species of cichlid
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69 AQKETYCLPNIGID 82
:|| || :: :|||
2 TQKITYRISGYGID 15
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Length 2610;

Search completed: Fri Jun Job time: 130 secs. 17:11:56



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fr1 Jun 11 17:20:38 1999; MasPar time 4.88 Seconds 65.330 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-2 (1-15) from US08991628.pep 105

Scoring table: PAM 150 Gap 15

Searched: 170751 segs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 37:part32 33:part33
34:part24 35:part35 36:part36 37:part37 38:part38

Mean 18.438; Variance 59.855; scale 0.308

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	1 5	14	13	12	11	10	9	8	7	σ	υ	4	ω	N		Result No.
U	57	57	57	57	57	57	57	82	84	. 86	86	105	105	105	105	Score
55.5	54.3	54.3	54.3	54.3	54.3	54.3	54.3	78.1	80.0	81.9	81.9	100.0	100.0	100.0	100.0	Query
433				796	796	796	693	560			19	999	614	30	15	Length
S	17	23	21	ø	ø	38	9	24	21	16	16	σ	19	16	20	DB
W41/32	R86866	W25636	W13134	R49730	R49731	W85598	R49732	W13009	W15489	R93962	R93961	R30742	W07908	R93960	W04842	Ħ
Arabidopsis chloropia	Human protocadherin p	Human cadherin-11.	Full length human cad	Sequence encoded by m	Sequence encoded by h	Cadherin-11.	Sequence encoded by h	Segment of desmosomal	Pemphigus foliaceus a	Peptide combining wit	Peptide combining wit	Human pemphigus vulga	Pemphigus vulgaris an	Peptide combining wit	Self epitope of desmo	Description
6.44e+01	5.11e+01	5.11e+01	5.11e+01	5.11e+01	5.11e+01	5.11e+01	5.11e+01	1.16e-01	6.96e-02	4.18e-02	4.18e-02	2.95e-04	2.95e-04	2.95e-04	2.95e-04	Pred. No.

4	4	4	. 4	4	4	ω	ω̈	ω	w	w	w	ω	w	31	ω	N	2	N	2	N	N	2	2	N	N	,_	_	-
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i surface	encoded by	Sequence encoded by T	laccase clon	Staphylococcus aureus	Product of alternativ	tively spli	Human protocadherin-4	ne	Cold acclimatization	sezia fun	Streptococcus pneumon	filamin.	Human cadherin-12.	Putative human cadher	Helicobacter pylori u	laccase c	ed by	rrheae pilC2	nce of human l	Human E-cadherin prec	Tobamovirus replicati	Human wild-type E-Cad	ide combining	Full length human cad	cadher	gillus sp.	ergillus	STITLE
		2.00e+02	2.00e+02	2.00e+02	•	.60e+0	.60e+0	.60e+0	•	.60e+0	ċ	.28e+0		e+0	.28e+0	.02e+0	.02e+0	.02e+0	.10€	.10e+0	.10e+0	.10e	.10e+0	.44e+0	.44e	.44e+0	.446	į

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derived from the juman desmoglein protein are described in W04841-47. Sequence 15 AA;	from the human desmoglein 3 protein (amino acids 9 implicated as a self epitope in pemphigus vulgaris.	T-cells in individuals with the autoimmune disease. This peptide is	protein, such as HLA-DR, which is associated with a human autoimmune	sequence corresponding to a sequence motif for a MHC class II	tolerising an individual to that polypeptide. In both cases, the	autoantigen; or an isolated human pathogen polypeptide capable of	protein	Claim 1; Page 38; Skpp; English. Pharmaceutical preparations for tolerisation to antigens comprise	auto-immune disease	and non-self antigens		Pemphigus vulgaris auto-antigens and multiple sclerosis non-self	/42.	STROMINGOT II. WICHESTE.	07-MAR-1995; US-400796.	07-MAR-1996; U03182.	12-SEP-1996.	W09627387-A1.	Homo sapiens.	influenza; haemagglutinin; reovirus; sigma protein.	human papillomavirus; Epstein-Barr virus; DNA polymerase;	pempnigus vulgaris; desmogiein; mulcipie scielosis;	autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;	Tolerisation; self-epitope; antigen; autoimmune disease;	Self epitope of desmoglein 3, implicated in autoimmune disease.		W104842 standard; peptide; 15 AA.	

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RESULT I LOUIS CONTROL OF THE PROPERTY OF THE 
FRESULT PRODUCT PRODUC
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A new peptide is disclosed which contains at least 5 contiguous amino acids from the sequence Val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Ala Ile Val Asp Arg Glu Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Ala Ile Val Asp Arg Glu Glu (the present sequence), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal
                                                            Fused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients wipemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fattal if untreated. The PV antigen was fused to a human IgGl hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-1996.
30-JUN-1995;
30-JUN-1994;
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18-MAY-1994; JP-129556.
(KURS ) KURARAY CO LTD.
WPI; 96-045392/05.
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Peptide combining with
anti-interepidermal cel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pemphigus vulgaris antigen protein extracellular region.
Autoantibody; immunoglobulin G; IgGl; fusion protein; di
treatment; pemphigus vulgaris; PV; bulla; blister; skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1997
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30 AA;
vulgaris.
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NO. 2.95e-04;
Mismatches 0;
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                                                                                                                                Example 1; Page 4; 7pp; Japanese.

New peptides are disclosed which contain at least 5 contiguous amino acids from the sequence val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe val Val Asp Ile Asp Ile Asn Ile Thr Ala Ile Val Asp Arg Glu Glu (see R93960), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal cellular antibody. The present sequence is a specific example of the new peptides.
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15-DEC-1992.
27-NOV-1991; ;
27-NOV-1991; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-interepidermal cellular antibody-combining peptide - whic be immobilised on column to form adsorbent useful for treating
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18-MAY-1994; JP-129556.
(KURS) KURARAY CO LTD.
WPI; 96-045392/05
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J07309893-A.
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Peptide combining with anti-interepidermal cellular antibody.
anti-interepidermal cellular antibody; autoantibody; adsorbent.
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Sequence 999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding pemphigus vulgaris a diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.
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keratinocyte cell su
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L8-MAY-1994;
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igus vulgaris; skin disease; autoantibodies;
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No. 2.95e-04;
No. 2.95e-04;
e 86; DB 16; L. No. 4.18e-02; Mismatches 0;
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Example 2; Page 5; 7pp; Japanese.

New peptides are disclosed which contain at least 5 contiguous amino acids from the sequence Val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Ala Ile Val Asp Arg Glu Glu (see R93960), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal cellular antibody. The present sequence is a specific example of the new peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J09077800-A.
25-MAR-1997.
12-SEP-1995;
12-SEP-1995;
pemphigus foliaceus antigen-IgG constant region fusion protein - lin through the hinge region used to treat pemphigus foliaceus Claim 1; Page 10-12; 17pp; Japanese.

This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion protein is immobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1994; 129556.
18-MAY-1994; JP-129556.
(KURS) KURARAY CO LTD.
WPI; 96-045392/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pemphigus foliaceus antigen-IgG constant region fusion p
Pemphigus foliaceus; autoantibody; constant region; IgG;
extracellular region; antigen; hinge portion; skin;
dermatitis herpetiformis; fusion protein; detection; ss.
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J07309893-A.
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18-MAY-1994;
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R WPI; 97-146518/14.

The Antibody reactive with part of desmosomal cadherin - exposed on purifice of epithelial or carcinoma cells, not bound to desmosomes, present for diagnosis and treatment of carcinoma micrometastases PS Claim 7; Page 5; Bpp; German.

CC The present sequence is a segment of the desmosomal cadherin (DC), CC desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) CC diagnose, i.e. to detect carcinoma cells, especially CC micrometastases, not bound to desmosomes, to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods and CC as a therapeutic to deliver agents, e.g. other Ab or toxins, to CC metastatic carcinoma, and detects parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the parts of DC that are not compared to the
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28-AUG-1992; JP-230028.
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Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithe carcinoma; desmosome; antibody; epitope; diagnosis; detectio micrometastasis; separation; enrichment; targetted delivery;
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osteogenesis;
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C line MG373-El and from mouse liver tissue, amplified by PCR, and
C then as much common DNA as possible removed by hybridisation between
C the 2 libraries. Residual El-specific DNA was amplified, inserted
C into lambda gt10 and screened by plaque hybridisation. A minibank of
C 273 E-specific clones was recovered, their inserts amplified and
C used to screen total RNA from both cell types. One clone specific
C for El was identified and sequenced. The insert from this clone was
C used to screen total RNA from El RNA and the longest posn, insert
C cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced;
it encoded the 796 AA mouse precursor protein (Q44391/R49730). The
C insert was also used to screen a cDNA bank prepd. from human
osteosarcoma to identify 2 clones encoding the 2 human precursor
proteins - OSF-4-1 and OSF-4-2 (Q44392/R49731 and Q44393/R49732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                           Assessing likelihood of successful pregnancy by measuring levels of cadherin-11 in endometrium - also diagnosis of infertility from low cadherin levels and increasing cadherin levels by administering progestin or cadherin-encoding DNA Disclosure; Page 54-57; 63pp; English.

The likelihood of establishing and maintaining a pregnancy, blastocyst implantation or endometrial receptivity are determined by measuring the level of cadherin-11 mRNA or protein in endometrial cells. A level below a standard value indicates inability to establish or maintain pregnancy. Women who are identified as having low level expression of cadherin-11 in endometrial cells can then be treated with a genetic construct comprising the cadherin-11 cDNA. The expression of cadherin-1 from the construct increases fertility and lessens the
                                                                                                                                                                                                                                                                                                       and receptiveness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V83124.
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(UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endometrium; trophoblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cadherin-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W85598 standard; protein; 796
W85598;
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                                                                                                                                                                                                                                                                                                          Cadherin-11 expression and receptiveness than
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CDNA libraries were constructed from the mouse osteoblast:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-1998; CA0397
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                                           IFVVDKNTGDIN 14
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im; trophoblast; balstocyst; infertility.
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larity 50.0%;
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larity 50.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                         Score 57; DB 38;
Pred. No. 5.11e+01;
5; Mismatches 1
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Pred. No. 5.11e+01;
5; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C CDNA libraries were constructed from the mouse osteoblastic cell (line MC3T3-El and from mouse liver tissue, amplified by PCR, and then as much common DNA as possible removed by hybridisation between the 2 libraries. Residual El-specific DNA was amplified, inserted into lambda 9t10 and screened by plaque hybridisation. A minibank of 273 E-specific clones was recovered, their inserts amplified and used to screen total RNA from both cell types. One clone specific come total RNA from both cell types. One clone specific clone was deto screen cDNA prepd. from El RNA and the longest posn. insert cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced; it encoded the 796 AA mouse procursor protein (Q44391/R4973). The insert was also used to screen a cDNA bank prepd. from human proteins - OSF-4-1 and OSF-4-2 (Q44392/R49731 and Q44393/R49732
                                                                                                                                                                                                                                                                           (FARH ) HOECHST JAPAN LTD.
Amann E. Kawai S. OkazaKi M
WPI: 94-076152/10.
N-PSDB: 044221
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09-MAR-1994.
25-AUG-1993;
28-AUG-1992;
then as much common DNA as possible removed by hybridisation between the 2 libraries . Residual E1-specific DNA was amplified, inserted into lambda gt10 and screened by plaque hybridisation. A minibank of 273 E-specific clones was recovered, their inserts amplified and used to screen total RNA from both cell types. One clone specific
                                                                                                                      encoding them Claim 1; Page 13-17; 34pp; English. Claim 1; Page 13-17; 34pp; English. cDNA libraries were constructed from the mouse osteoblastic cell line MC3T3-E1 and from mouse liver tissue, amplified by PCR, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-1994 (first entry)
Sequence encoded by murine OSF-4 cDNA.
OSF-4; cadherin; growth factor; osteogenesis; osteoblast; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bone related, cadh and diagnosis of bone
                                                                                                                                                                                                                            New bone related, cadherin-like OSF-4 proteins and diagnosis of bone metabolic disease, and nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R49730;
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Claim 1; Page
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Amann E, Kawai S, Okazal
WPI; 94-076152/10.
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R49731;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                               25-AUG-1993;
28-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            796 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry) coded by human (dherin; growth:
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bone metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takeshita S,
                                                                                                                                                                                                                                                                                                                             Takeshita
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Best Local :
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17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
(DOHE-) DOHENY EYE INST.
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19-APR-1993;
26-JAN-1994;
                                  08-JUL-1997.
17-APR-1992;
19-APR-1993;
17-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is full length human cadherin-11, which is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA used from a foetal brain cDNA library, using probes based on homologous rat cadherin cDNA.

Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expressic and antagonise its ligand/antiligand binding activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Full length human cadherin-11.
Ca2+ dependent; cell adhesion protein; foetal; cadherin; brain; human; antibody; purification; determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for El was identified and sequenced. The insert from this clone was used to screen cDNA prepd. from El RNA and the longest posn. insert cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced; it encoded the 796 AA mouse precursor protein (p44391/R49730). The insert was also used to screen a cDNA bank prepd. from human osteosarcoma to identify 2 clones encoding the 2 human precursor proteins - OSF-4-1 and OSF-4-2 (q44392/R49731 and q44393/R49732
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Sequence 796 AA;
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W25636;
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N-PSDB; T61925.
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                                                                                                                                                                                    US5646250-A.
                                                                                                                                                                                                                                                     Human cadherin-11.

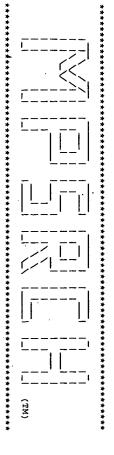
Human; cadherin; rat; calcium-dependent cell adhesion superfamily; cytoskeleton; eatenin; cancer.
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US-332638.
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larity 50.0%;
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No. 5.11e+01;
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5.11e+01;
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                                                                                 Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities claim 16; Page 122-125; 146pp; English.

Claim 16; Page 122-125; 146pp; English.

C R86865-R86867 represent the sequences for three protocadherins. This sequence represents the human protocadherin pc4. These sequences are related to cadherin, and possess cell adhesive ability. Cadherins are glycosylated integral membrane proteins that are involved in cell-cell adhesion. Cadherins are composed of an N-terminal extracellular domain which consists of 5 unique subdomains, a membrane spanning domain, and a c-terminal cytoplasmic domain. The cytoplasmic domain interacts with the cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain.

These sequences were isolated using primers 1 and 2 (see 703575 and the cell-cell adhesive properties. Antibodies produced against these composes are properties. Antibodies produced against these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents human cadherin-1 provides details of human cadherin-5, -8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human and rat cadherin polypeptide(s) - Claim 1; Column 89-94; 56pp; English.
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N-PSDB; T03573.
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   protocadherins, and Sequence 797 AA;
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W09600289-Al.
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                                                              sequences are useful for modulating the binding activity of
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                                can be
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d. No. 5.11e+01;
Mismatches 1;
                                therapeutically.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:18:54 1999; MasPar time 4.32 Seconds 139.098 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-2 (1-15) from US08991628.pep 105 1 FGIFVVDKNTGDINI 15

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 26.793; Variance 39.116; scale 0.685

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22222214 3222222222222222222222222222222	Result
1 5 5 5 5 5 5 5 5 5 5 5 5 5	Score
100.0 80.0 78.1 78.1 62.9 62.9 61.9 61.9 61.9 61.9 58.1 57.1 57.1 57.1 57.1 57.1 57.1 57.1 57	% Query Match
999 1043 1043 11043 1107 761 785 785 785 786 840 840 840 840 840 840 1612 1626 94 214 214 215 1626 624 624 624 624 624 624 624 624 624	Length
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desmoglein 3 precurso desmoglein 1 precurso desmoglein 1 precurso desmoglein 2 - human desmocollin 1a - bovi cadherin -7 - chicken desmocollin 1b precur desmocollin 1b precur desmocollin 1b precur desmocollin 1b precur desmocollin 1a precur Dscla precursor - hum DNA topoisomerase (AT D	Description
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sucrose alpha-glucosi	sucrose alpha-glucosi	180K protein - tomato	botulinum neurotoxin-	E-cadherin precursor,	cadherin-6B - chicken	hypothetical protein	hypothetical protein	hypothetical protein	cadherin 13 precursor	protein-tyrosine kina	E-cadherin precursor,	.probable lipoprotein	OB-cadherin precursor	cadherin-11 - mouse	cadherin 11 precursor	cadherin-11 - mouse	tldD homolog PH0246 -	ribonuclease hii - He	1	polyprotein - parsnip	bu brococamier in acou
2.18e+01	2.18e+01	2.18e+0	2.18e+0	2.18e+0:	2.18e+01	2.18e+01	2.18e+01	1.48e+01	1.48e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.00e+0	1.00e+0	1.00e+01	1.00e+0	1.00e+01	1.00e+0	6.75e+00	

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Query Match Best Local Sim Matches 15;	640-999 910-938 937-966 110,180,545 SUMMARY	50-615 52-157 160-267 270-383 390-495 496-598 616-639	FEATURE 1-23 24-49 50-999	GENETICS #gene #gene #cross-references #map_position 18q12.1 CLASSIFICATION #superf: KEYWORDS calcium	#journal Cell (199 #title Autoantib pemphig #cross-references MUID: #accession A41088 #accession E41089 ##cross-references G ##cross-references G	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors
y Match 100.0%; Score 105; DB 1; Length 999; Local Similarity 100.0%; Pred. No. 1.59e-09; hes 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	intracellular #status predicted #label desmoglein repeat #label DG1\ desmoglein repeat #label DG2\ g_site carbohydrate (Asn) (covalent) #stoted cted #molecular-weight 107502 #checksum 831	extracellular #status predicted #label cadherin repeat homology #label CR1\ cadherin repeat homology #label CR2\ cadherin repeat homology #label CR3\ cadherin repeat homology #label CR3\ cadherin repeat homology #label CR4\ cadherin repeat homology #label CR5\ transmembrane #status predicted #label	n si n pr	GDB:DSG3 18q12.1-18q12.2 18q12.1-18q12.2 superfamily cadherin, cadherin calcium binding, cell adhesion; transmembrane protein	Title Autoantibodies against a novel epithelial cadherin in Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion. Cross-references MUID:92069753 accession A41088 ###nolecule_type mRNA ##residues 1-999 ##label AMA ##residues 1-999 ##label AMA	IJHUG3 #type complete desmoglein 3 precursor - human pemphigus vulgaris antigen #formal_name Homo saplens #common_name man 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 18-Sep-1998 A41088 A41088 A41088 A41088 A41088 A41088 A41088 A41088

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ACCESSIONS
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                                                                                                                                                                                                                           Zimbelmann, R.; Franke, W.W.

#journal Eur. J. Cell Biol. (1990) 53:1-12

#title Identification of desmoglein, a constitutive desmosomal

#lycoprotein, as a member of the cadherin family of cell

adhesion molecules.

#cross-references_MUID:91168965
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#title Desmoglein shows extensive homology to the cadherin family
coll adhesion molecules.

#cross-references MUID:91097553

#accession A37785
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#title Complete amino acid sequence of the epidermal desmoglein
precursor polypeptide and identification of a second to
of desmoglein gene.
#cross-references MUID:92037656
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                                                                                            ##residues 44-1001,'AOPPSAT' ##label KO3
##cross-references GB:X57784
this sequence has been revised
$38721
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##cross-references GB:S64268; GB:S64270
NCE 12770c
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desmoglein BDGM
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1993 #sequence_revision 30:Jun-1993 #text_change
05-Sep-1997
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#superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
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#title Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, is related to the cadherin family cell adhesion molecules.

#cross-references_MUID:91271279
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J. Cell Sci. (1991) 99:809-821
Structural analysis and expression of human desmos cadherin-like component of the desmosome.
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Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Rees, D.A.; King, I.A.; Magee, A.I. Blochem. Soc. Trans. (1991) 19:1060-1064 Desmosomal glycoproteins I, II and III: nov
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#map_position 18q12.1-18q12.2
CLASSIFICATION #superfamily cadherin; cadherin
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#cross-references MUID:92037656
#accession B38872
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#cross-references MUID:92175187
#accession A61279
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##cross-references GB:S64273
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##residues 1-55 ##label WH3
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CLASSIFICATION #superfamily cadherin; cadherin
KEYWORDS calcium binding; cell adhesion;
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#title Cloning and sequence analysis of desmosomal glycoproteins and 3 (desmocollins): cadherin-like desmosomal adhesion molecules with heterogeneous cytoplasmic domains.
#cross-references MIID:91185414
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                                                                                                   ##molecule_type protein
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##experimental_source nasal epidermis
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J. Cell Sci. (1990) 97:339-246
Desmosomal glycoproteins 2 and 3 (desmocollins) show N-terminal similarity to calcium-dependent cell-cell
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Differentiation (1991) 47:29-36
Amino acid sequence of bovine muzzle epithelial desmocollin
derived from cloned cDNA: a novel subtype of desmosomal
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#journal Development (1995) 121:1321-1332
#title Neural crest cell-cell adhesion controlled by sequential
#title subpopulation-specific expression of novel cadherins.
#cross-references MUID:95309115
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                                                                                                                                                                                                                                                                                                                                     ##residues 1-785 ##label NAK
##cross-references GB:D42150; NID:9868000; PID:9868001
##cross-references GB:D42150; NID:9868000; PID:9868001
##crosidues 1-785 #molecular-weight 87171 #chec
XY #length 785 #molecular-weight 87171 #chec
                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                     Local Similarity
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Local Similarity 53.8%;
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                                      1JBODF *type complete desmocolin 1b precursor - bovine desmosomal glycoprotein 3 *formal_name Bos primigenius taurus *common_name cattle 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change 24-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150180 #type complete
cadherin-7 - chicken
#formal_name Gallus gallus #common_name chicken
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
09-May-1997
                                                                                                                                                                                                                                                                 62.9%;
larity 61.5%;
Conservative
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#binding_site phosphate (Thr) (covalent) (by casein
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#binding_site phosphate (Ser) (
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kinase C) #status predicted
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#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
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cadherin repeat homology #label CR2\
cadherin repeat homology #label CR3\
cadherin repeat homology #label CR4\
cadherin repeat homology #label CR4\
cadherin repeat homology #label CR5\
transmembrane #facture
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Pred. No. 2.45e-01;
4; Mismatches 1;
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Pred. No. 2.45e-01
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#gene
CLASSIFICATION
KEYWORDS
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##cross-references GB:M67489; GB:M61750; NID:g162970; PID:g162971
##note part of this sequence, including the amino end of the
mature protein, was confirmed by protein sequencing
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##cross-references GB:X56966; NID:g315; PID:g316
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Local Similarity 53.8%;
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                                            15-Aug-1997 #sequence_revision B48910
                                                                                                B48910 #type fragment
desmocollin 1b precursor - human (fragment)
#formal_name Homo sapiens #common_name man
08-Dec-1995 #sequence_revision 08-Dec-1995
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J. Cell Biol. (1991) 113:381-391
Cloning and sequence analysis of desmosomal glycoproteins and 3 (desmocollins): cadherin-like desmosomal adhesion molecules with heterogeneous cytoplasmic domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mechanic, S.; Raynor, K.; Hill, J.E.; Cowin, P. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4476-4480 Desmocollins form a distinct subset of the cadherin family of cell adhesion molecules.
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alternative splicing; calcium binding; cell adhesion;
duplication; glycoprotein; phosphoprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #length 839
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kinase II) #status predicted
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kinase C) #status predicted\
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#domain propeptide #status predicted #label PRO\
#product desmocollin 1b #status experimental #label MAT\
#domain extracellular #status predicted #label EXT\
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domain intracellular #status predicted #label INT\
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     Arnemann,
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; Garrod, D.R
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Pred. No. 2.45e-01
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  Spurr,
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N.K.; Buxton,
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67-172
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67-172
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#map_position 18q12.2-18q12.2

CLASSIFICATION *superfamily cadhe;

KEYWORDS alternative splici
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#title Cloning of the cDNA (DSC1) coding for human type
desmocollin and its assignment to chromosome 18
#cross-references MUID:94116981
                                                                                                                                                                                                                                                                                                                                                                                                                        #gene
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#accession A48910
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##residues
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Similarity 53.8%;
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#superfamily cadherin; cadherin repeat homology
alternative splicing; calcium binding; cell adhesion;
glycoprotein; phosphoprotein; transmembrane protein
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Cloning of the cDNA (DSCI) coding for human type 1
desmocollin and its assignment to chromosome 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A48910 #type fragment desmocollin la precursor - human (fragment) #formal_name Homo sapiens #common_name man 08-Dec-1995 #sequence_revision 08-Dec-1995
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137281 #type complete
Dsc1a precursor - human
#formal_name Homo sapiens #common_name man
12-Aug-1996 #sequence_revision 12-Aug-1996
16-Feb-1997
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#length 770 #checksum 4861
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#length 824 #checksum 2645
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                                                                                                                                                                                                                           53.8%;
                                                                                                                                                                                                                           Score 65; DB 2; I
Pred. No. 3.76e-01;
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Pred. No. 3.76e-01
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                                                                                                                                                                                                             4; Mismatches
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Best Local Similarity 53.8%;
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Best Local
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#journal Int. J. Dev. Biol. (1993) 37:101.110

#title Differential synthesis of type 1 and the synthesis of type 1 and the synthesis of type 1 and the synthesis of type 2 and the synthesis of type 3 and the synthesis of type 1 and the synthesis of type 3 and the
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#journal Int. J. Dev. Biol. (1993) 37:101-110
#title Differential synthesis of type 1 and type 2 desmocollin
#cross-references MUID:93283249
#accession 137281
#authors Dereuddre, S.; Frey, S.; Delaporte, C.; Jacquemin-Sablon, #journal Biochim. Blophys. Acta (1995) 1264:178-182

*title Cloning and characterization of full-length cDNAs coding in the DNA topoisomerase II beta from Chinese hamster lung cells sensitive and resistant to 9-OH-ellipticine.

*cross-references MUID:96085121

*accession $59969
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IFICATION #superfamily cadherin; cadherin repeat homolo
RY #length 840 #molecular-weight 93848 #checks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 FNLFYIEKDTGDI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##status preliminary; translated
##molecule_type mRNA
##residues 1-894 ##label RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 61.9%;
Similarity 53.8%;
                                                                                                                                                                                                                                                                                                         S59969 *type complete
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) isoform
beta - Chinese hamster
DNA topoisomerase II isoform beta; DNA-gyrase
#formal_name Cricetulus griseus #common_name Chinese hamster
15-Feb-1996 *sequence_revision 13-Mar-1997 *text_change
17-Mar-1999.
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#formal_name Homo sapiens #common_name man
12-Aug-1996 #sequence_revision 12-Aug-1996
16-Feb-1997
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Pred. No. 3.76e-01;
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Pred. No. 3.76e-01

    Mismatches

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Best Local Similarity 72.7%;
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#Journal Nucleic Acids Res. (1992) 20:5587-5592
#title Isolation of cDNA clones encoding the beta isozyme of human DNA topoisomerase II and localisation of the gene to chromosome 3p24.
#cross-references MUID:93087165
#accession $26730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Chung, T.D.Y.; Drake, F.H.; Tan, K.B.; Per, S.R.; Crooke, S.T.; Mirabelli, C.K.

#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:9431-9435

#title Characterization and immunological identification of cDNA 
#cross-references encoding two human DNA topoisomerase II isozymes.
                                                                                                                                                                                                                                   #authors Austin, C.A.; Fisher, L.M.
#journal FEBS Lett. (1990) 266:115-117
#title Isolation and characterization of a human cDNA clone encoding
#cross-references MUID:90306333
#accession S10710
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#cross-references
                                                                     #title
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                                                                                                                    authors
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NCE A39242
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##cross-references EMBL:X86455; NID:g790987; PID:g790988
##experimental_source lung
                                                                                                                                                                ##molecule_type mRNA
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DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) beta,
splice form 2 - human
DNA topoisomerase II isoform beta-2
DNA topoisomerase II isoform beta-1
#formal_name Homo sapiens #common_name man
04-0ct-1991 #sequence_revision 03-May-1996 #text_change
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DNA topoisomerase (ATP-hydrolyzing) medium chain homology
ATP; DNA binding; DNA replication; isomerase; nucleus
                                      Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M.
Blophys. Acta (1993) 1172:283-291
Novel HeLa topoisomerase II is the II-beta isoform: complete coding sequence and homology with other type II
                                                                                                                                                                                                                                                                                                                                                                                                 S10710
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    medium chain homology #label TOP
jth 1612 #molecular-weight 182074 #checksum 5332
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es EMBL:X68060; NID:g37230; PID:g37231
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Pred. No. 2.01e+00;
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KEYWORDS
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GENETICS
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Best Local
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                                                                                                                                                                                                   #journal
#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Davies, S.L.; Jenkins, J.R.; Hickson, J
#journal Nucleic Acids Res. (1993) 21:3719-3723
#title Human cells express two differentially
topoisomerase II-beta mRNA.
#cross-references_MUID:93376494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #accession
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                                                                                                                                                                               #title The complete genome sequence of #cross-references MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .934 IFVVDRNTVEI 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references GDB:131575; OMIM:126431
p_position 3p24-3p24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
##residues 24-80 ##label DAV
##cross-references EMBL:X71911
##note this sequence represents a
designated beta-2
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1-23,29-1610,'A',1612-1626 ##label AU2
##cross-references EMBL:Z15111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 596-1430,'S',1432-1610,'A',1612-1626 ##label AU1 ##cross-references EMBL:Z15115; NID:g288564; PID:g288565
                                                                   ##molecule_type DNA 1-94 ##label BLAT
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                                    ##cross-referenges GB:AE000421; GB:U00096;
UWGP:b3446
                ##experimental_source
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Similarity 72.7%;
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DNA topoisomerase (ATP-hydrolyzing) medium chain homology
alternative splicing; ATP; dimer; isomerase; nucleus
                                                                                                                                                                                                                                                                                                                                                                              Abb141 #type complete
hypothetical 10.6 KD protein in gntR-ggt in
Escherichia coli (strain K-12)
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997
14-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M. submitted to the EMBL Data Library, September 1992
                                                                                                                                                                                                                                                          Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao
                                                                                                                                                            A65141
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medium chain homology #label TOP
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                                                                                                                                       preliminary; nucleic acid sequence
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Pred. No. 2.01e+00;
                   K-12,
                substrain
                                                         NID:g1789854; PID:g1789855;
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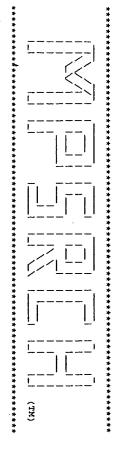
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ORGANISM
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ENTRY
TITLE
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SUMMARY
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                                                                           Best Local Similarity 42.9%;
Matches 6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.1%;
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                  Yasuda, M.; Tabata, S.

#Journal DNA Res. (1996) 3:109-13.

Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions.
                                                                                                                                                                       ##status preliminary
##molecule_type DNA
1-214 ##label KAN
##cross-references EMBL:D64000; GB:AB001339; NID:g1001484; PID:d1010882;
##cross-references EMBL:D640001603
PID:g1001603
the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
Library, June 1996
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4 FVVDKNTGDIN 14
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1 FGIFVVDKNTGDIN 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S76379 #type complete
hypothetical protein - Synechocystis sp. (strain PCC 6803)
#formal_name Synechocystis sp.
PCC 6803
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#length 94 #molecular-weight 10613 #checksum 4152
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Pred. No. 3.02e+00;
7; Mismatches 1
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Search completed: Fri Jun 11 17:20:20 1999 Job time : 86 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:16:04 1999; MasPar time 2.46 Seconds 172.535 Million cell updates/sec

Tabular output not generated.

Sequence: 1 FGIFVVDKNTGDINI 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37

swiss-prot37 1:swissprot

Statistics: Mean 27.494; Variance 34.835; scale 0.789

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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HYPOTHETICAL 81.7 KD P	T-CADHERIN PRECURSOR (PROTEIN DISULFIDE ISOM	CELL DIVISION PROTEIN	MACROPHAGE - STIMULATING	EPITHELIAL-CADHERIN PR	CADHERIN-11 PRECURSOR	CADHERIN-11 PRECURSOR	RIBONUCLEASE HII (EC 3	GENOME POLYPROTEIN [CO	CADHERIN-14 PRECURSOR.	HYPOTHETICAL 10.6 KD P	DNA TOPOISOMERASE II,	DNA TOPOISOMERASE II,	DNA TOPOISOMERASE II,	DNA TOPOISOMERASE II,	DESMOCOLLIN 1A/1B PREC	1B	DESMOCOLLIN 1A/1B PREC	DESMOGLEIN 2 PRECURSOR	DESMOGLEIN 1 PRECURSOR	DESMOGLEIN 1 PRECURSOR	DESMOGLEIN 3 PRECURSOR	Description
5.10e+00	5.10e+00	5.10e+00	5.10e+00	3.30e+00	3.30e+00	3.30e+00	3.30e+00	3.30e+00	2.12e+00	8.60e-01	8.60e-01	5.44e-01	5.44e-01	5.44e-01	5.44e-01	5.44e-01	8.27e-02	5.11e-02	1.34e-05	4.50e-06	4.50e-06	2.66e-11	Pred. No.

EMBL; M76482; G190752; -.

PIR; A41088; IJHUG3.

MIM; 165615; -.

PROSITE; PS00232; CADHERIN; 3

PFAM; PF00028; cadherin; 4.

HSSP; P09803; 1EDH.

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BRAIN-CADHERIN PRECURS	ACYL-COENZYME A OXIDAS	HYPOTHETICAL PROTEIN M	TOPOISOMERASE IV SUBUN	DI-/TRIPEPTIDE TRANSPO	TROPONIN C, BODY WALL	HYPOTHETICAL 38.5 KD P	28 KD OUTER MEMBRANE P	HYPOTHETICAL 19.5 KD P	SUCRASE-ISOMALTASE, IN	SUCRASE-ISOMALTASE, IN	PUTATIVE RNA-DIRECTED	BOTULINUM NEUROTOXIN T	AMINOPEPTIDASE N (EC 3	EPITHELIAL-CADHERIN PR	EPITHELIAL-CADHERIN PR	PLACENTAL-CADHERIN PRE	CADHERIN-6 PRECURSOR (CADHERIN-6 PRECURSOR (B-CADHERIN PRECURSOR (HYPOTHETICAL 62.8 KD T	CADHERIN-10 PRECURSOR.
1.82e+01	1.82e+01	1.82e+01	1.82e+01	1.82e+01	1.82e+01	1.20e+01	1.20e+01	1.20e+01	7.84e+00	7.84e+00	7.84e+00	7.84e+00	7.84e+00	7.84e+00	7.84e+00		7.84e+00	7.84e+00	7.84e+00	7.84e+00	5.10e+00

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6482; G190752;	or send an email to licenseeisp-sip.cn).	s requires a	modified and this statement is not removed. Usage by and for commercial	European Bioinformatics Institute. There are no restrictions on	between the Swiss Institute of Bioinformatics and the EMBL outstation	This SWISS-PROT entry is copyright. It is produced through a collaboration		DESMOSOMAL SUBFAMILY.	- STATIARITY: RETONGS TO THE CADHERIN FAMILY. BELONGS TO THE	LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES	DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THE	PHIGUS VULGARIS (PV) IS	(POTENTIAL).	CARCINOMAS.	-!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND		MEDIATING CELL-CELL ADHESION.	INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE	EINCHTON: COMPONENT OF	Vilgaris, a disease of cell addesion.";	"Autoantibodies against a novel epithelial cadherin in pemphigus	., STANLEY J.R.;	MEDLINE; 92069753.	SEQUENCE FROM N.A.	[1]	EUNARIOTA; METACOA; (HORDATA; VERIEDRATA; MENERALIA; ECIBERTA; DETMATEG: CATABERTAT: HOMINITAET HOMO	Waller Ta		ω	01-001-1993 (REL. 27, MAST SEQUENCE OFDETE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDETE)	01-0CT-1993 (REL. 27, CREATED)	P32926;	LT 1 DSG3_HUMAN STANDARD; PRT; 999 AA.

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Q03763;
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CARBOHYD
CARBOHYD
SEQUENCE
SEQUENCE OF 44-493 FROM N.A.

MEDLINE; 91097553.

GOODWIN L., HILL J.E., RAYNOR K., RASZI L., MANABE N
GOODWIN L., HILL J.E., RAYNOR K., RASZI L., MANABE N
PDESMOGICEL SHOWS EXTENSIVE homology to the cadherin
adhesion molecules.";
BIOCHEM. BIOPHYS. RES. COMMUN. 173:1224-1230(1990).
BIOCHEM. BIOPHYS. RES. COMMUN. 173:1224-1230(1990).
-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME:
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS /
FILAMENTS MEDIATING CELL-CELL ADHESION.
                                                                                                                              MEDLINE; 9203
KOCH P.J., GO
FRANKE W.W.;
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BOS TAURUS (BOVINE).
THE ARYOTA; METAZOA;
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TRANSMEM
DOMAIN
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"Identification of desmoglein,
glycoprotein, as a member of th
molecules.",
EUR. J. CELL BIOL. 53:1-12(1990)
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CARBOHYD
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01-OCT-1993 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                 "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene."; poly. J. CELL BIOL. 55:200-208(1991).
                                                                                                                                                                                                                                                                              SUBMITTED
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                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
ISSUE-MUZZLE EPITHELIUM;
OCH P.J., GOLDSCHMIDT M.D.,
UBMITTED (MAR-1991) TO EMBL
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Similarity 100.0%;
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ANTIA; PECORA; BOVOIDEA; BOVIDAE;
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LAST SEQUENCE UPDATE)
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R (DESMOSOMAL GLYCOPROTEIN I)
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Pred. No. 2.66e-11;
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TISSUE-KERATINOCYTES;
MEDLINE; 91271279_.
WHEELER G.N. PARKER A.E.,
ARNEMANN J., RUTMAN A.J., P.
BUXTON R.S., MAGEE A.I.;
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01-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                            EUKARYOTA;
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                                                                                                                                                                      PRIMATES;
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                                                                                                                          EQUENCE FROM N.A.
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TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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RYOTA; METAZOA; CHORDATA; VERTEBRATA;
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3 (REL. 27, L)
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Pred. No. 4.50e-06;
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T 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TTCMOGLEIN 2 PRECURSOR (HDGC).
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Matches 9; Conse
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INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDI
FILAMENTS MEDIATING CELL-CELL ADHESION.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND OESOPHAGUS.
-!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
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MIM; 125670;
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SIMILARITY: BELONGS TO THE
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No. 4.50e-06;
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MIM; 125671; -
PROSITE; PS002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHAEFER S., KOCH P.J., FRANKE W.W.;
"Identification of the ubiquitous human
expression catalogue of the desmoglein s
cadherins.";
                                                                                                                                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete amino acid sequence of the epidermal desm
polypeptide and identification of a second type of
EUR. J. CELL BIOL. 55:200-208(191).
-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS
                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                                                                                                                                          SEQUENCE
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                                        98 FGIFVFNKDTGELNV 112
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINOMAS.
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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FGIFVVDKNTGDINI
                                                                             Similarity 60.0% 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RES. 211:391-399(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G416178;
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e of the
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DESMOGLEIN 2.
EXTRACELLULAR
                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                 DB 1;
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  of desmoglein gene.";
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                                                                               Indels
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AND INTERMEDIATE
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Q01107; Q28095;
01-FEB-1994 (REI
01-FEB-1994 (REI
15-DEC-1998 (REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adhesion molecules.";
PROC. NATL. ACAD. SCI
                     This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Desmosomal glycoproteins 2 and 3 (desmocollins) show N-terminal similarity to calcium-dependent cell-cell adhesion molecules."; CELL SCI. 97:239-246(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MECHANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 133-155.
MEDLINE; 91115997.
HOLTON J.L., KENNY T.P.,
SHARMA R., GARROD D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIOM CLONEC CDNA: a novel subtype DIFFERENTIATION 47:29-36(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91185
COLLINS J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-EPIDERMIS;
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EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                         PARRISH E.P., MARSTON GARROD D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (18),
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                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANKE W.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOCH P.J., GOLDSCHMIDT M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=MUZZLE EPITHELIUM;
MEDLINE; 92008912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 133-893 FROM
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MECHANIC S., RAYNOR K.,
"Desmocollins form a di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. CELL BIOL. 113:381-391(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARTIODACTYLA;
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                                                                                                                                                                                                                                                                                                                                                        "Size heterogeneity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and sequence analysis (desmocollins): cadherin-like c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence
rom cloned cDNA: a n
                                                                                                                                                                                     E desmosomal glycoproteins 2 and 3 (desmocollins) in MDCK cells.";

CELL SCI. 96:239-248 (1990).

FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSTTIONLING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES.

TO THE KERATINIZATION OF EPITHELIAL TISSUES.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: EPIDERMIS AND WEAKLY IN TONGUE PAPILLAE.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                            PTM: FORM 1A IS PHOSPHORYLATED ON A SERINE BUT FORM 1B IS NO ALTERNATIVE PRODUCTS: TWO FORMS; 1A OR DG2 (SHOWN HERE) AND DG3; ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE
                                                                                                    DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91185414.
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RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28, CREATED)
28, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
PRECURSOR (DESMOSOMAL GLYCOPROTEIN
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         institutions as long atement is not removed.
                                                                                                                                                                                                                                                                                                                                     phosphorylation and transmembrane organisation roteins 2 and 3 (desmocollins) in MDCK cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of bovine muzzle epithelial novel subtype of desmosomal
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                                                                                                                                                                                                                                                                                                                                                                                    MATTEY D.L., MEASURES H.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subset of the cadherin family of cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COWIN P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l desmocollin derived
cadherins.";
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                                                      a collaboration - MBL outstation -
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01-NOV-1997
15-DEC-1998
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SEQUENCE
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DOMAIN
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                                                                                                                  MEDLINE; 93283249.
THEIS D.G., KOCH P.J., FRANKE W.W.;
"Differential synthesis of type 1 an
human stratified epithelia.";
INT. J. DEV. BIOL. 37:101-110(1993).
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REPEAT
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   SEQUENCE FROM N.A.
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             EUKARYOTA;
                                                                                                                                                                                                                                                                                                                               DESMOCOLLIN
                                                                                                                                                                                                                                                                                                                                                                                               208554;
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                                                                                                                                                                                                                                                             PRIMATES;
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                                                                  (SSUE=FORESKIN;
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A43838;
A39377;
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X58029; G453584; -.
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X56968; G314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M67489; G162971;
X56966; G316; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                           CATARRHINI;
                                   (JUN-1994)
                                                                                                                                                                                                                                                                          NS (HUMAN).
METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   email
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(REL.
(REL.
1A/1B
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                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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dherin; 4.
                                                                                                                                                                                                                                                                                                                             PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192
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ω
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53.8%;
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                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                           HOMINIDAE;
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                                   EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₩,
                                                                                                                                                                                                                                                                                                                             (DESMOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB 1; I
Pred. No. 5.11e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B/DG3).
MISSING (IN FORM 1B/DG3).
T -> A (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION; TRAN
1-BINDING; ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVYLCGQDEEH ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                     type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                             MAMMALIA; EUTHERIA
                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESIRGHTLVKN
                                                                                                                                                       desmocollin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE;
ATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local
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MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERNAL CELL
POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED
TO THE KERATINIZATION OF EPITHELIAL TISSUES.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I. TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EPIDERMIS, LESS IN LYMPH
NODE AND TONGUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Keratinization is associated with the express; related to the desmosomal cadherins DGII/III."; FEBS LETT. 286:9-12(1991).
-i- FUNCTION: COMPONENT OF INTERCELLHIAD PROPERTY IN THE INTERCELLHIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                 VARSPLIC CONFLICT
                                                                                                                                                    CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                  MIM; 125643; -.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z34522; G505538; -. EMBL; Z34522; G505537; -. EMBL; X72925; G457463; -. EMBL; X72925; G457464; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KING I.A., ARNEMANN J., SPURR N.K., "Cloning of the cDNA (DSC1) coding its assignment to chromosome 18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-SKIN;
MEDLINE; 94116981
                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                           HSSP; P09803;
CELL ADHESION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 135-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOMICS 18:185-194(1993).
                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                              CYTOSKELETON;
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                    SEQUENCE
                                                                                                                                                                                         REPEAT
                           182 FNLFYIEKDTGDI 194
                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:
DG3; ARE PRODUCED BY I
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: CALCIUM MAY BE BOUND BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESMOSOMAL SUBFAMILY.
   FGIFVVDKNTGDI
                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91323543
                                                  61.9%;
llarity 53.8%;
Conservative
                                                                                                                 841
132
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                                                                                                                                                                                                                                                                                                                              CALCIUM-BINDING;
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K
                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN;
                                                                                                                894
132
                                                                                                                                                    3542
3542
354
471
575
582
165
846
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                                                                                                    100044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : TWO FORMS; 1A OR DG2 (SHOWN HERE) AND ALTERNATIVE SPLICING OF THE SAME GENE. TO THE CADHERIN FAMILY. BELONGS TO THE
                                                                                                     ¥.
                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                               ω.
                                                                                                                                                                                     CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
                                                                                                                                                                                                                                                                                                                            TRANSMEMBRANE; REPEAT; SIGNAL; G; ALTERNATIVE SPLICING.
                                                                                                              MISSING (IN FORM 1B/DG3).
T -> S (IN REF. 3).
                                                                                                                                                    KVYLCGQDEEH -> ESIRGHTLIKN
                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                        DESMOCOLLIN 1A/1B
                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                         1B/DG3
                                                                                                    A287BCA9 CRC32;
                                                    Mismatches
                                                               No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the expression of DGII/III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BUXTON R.S.;
                                                                 œ
                                                                DB 1; I
8.27e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human type 1 desmocollin and
                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                          Length 894;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEATS
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                                                    0,
                                                                                                                                                      FORM
                                                    Gaps
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01-NOV-1997
01-NOV-1997
15-JUL-1998
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SPLICING OF T
-!- SIMILARITY: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSC1.
MUS MUSCULUS (MOUSE).
TITKARYOTA; METAZOA; C
 CARBOHYD
CARBOHYD
CARSPLIC
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN THE INTERACTION OF INTERCELLULAR DESMOSOME JUNCTIONS, INVOLVED IN THE INTERACTION OF PLAQUE POTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION, MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES.

1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHOI
RODENTIA; SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSC1_MOUSE
                                                                              REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P55849;
                                                                                                                                                                                                                                                                               EMBL; X97986; E246528; -. EMBL; X97986; E246529; -.
                                                                                                                                                                                                                                                                                                                                     use by non-profit institu
modified and this statement
                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The European Bioinformatics Institutes as long use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96420658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESMOCOLLIN
                                                         CARBOHYD
                                                                      CARBOHYD
                                                                                                                                         DOMAIN
                                                                                                                                                             DOMAIN
                                                                                                                                                                         CHAIN
                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                              PFAM
                                                                                                                                                                                                                                                                 MGD; MGI:109173; DSC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            j. INVEST. [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression of the 'skin-type' desmos
                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression of the 'skin-type' desmosomal cadherin inked to the keratinization of epithelial tissues
                                                                                                                                                                                                                                                                                                                                                                                                         DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                        ADHESION;
                                                                                                                                                                                                                                 P09803
                                                                                                                                                                                                                                            PS00232; CADHERIN; 00028; cadherin; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DERMATOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL.
(REL.
(REL.
1A/1B
                                                                                                                                                                                                                                           cadherin;
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    THE SAME GENE.
BELONGS TO THE CADHERIN FAMILY. BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-SKIN;
                                                                                                                                                                                                             REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35, CREATED)
35, LAST SEQUENCE UP
36, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRECURSOR.
                       886
242
354
471
575
582
130
145
546
613
  886
98953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHORDATA; VERTEBRATA; MAMMALIA;
[HI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107:531-538(1996)
                                                                                                                                                                                                          TRANSMEMBRANE; CYTOSKELETON; GLYCOPROTEIN; ; ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                           FORMS
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                                                                                                                                                                                                                                                        ν.
                                                                                                                                                                                                                                                                                                                                        is not removed.
                                                                             CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
POTENTIAL.

POTENTIAL.

KVYLCGQAEEH -> ESIRGHTLIKN

MISSING (IN FORM 1B).

6C3C94BA CRC32;
                                                         POTENTIAL
                                                                      POTENTIAL.
                                                                                                                                                     POTENTIAL
                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                          DESMOCOLLIN 1A/1B
                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                   It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSC1 is closely during mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA;
                                                                                                                                                                                                                                                                                                                                        λą
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                         (IN FORM 1B).
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Query Match Best Local

Similarity

58.1%; 46.2%;

Score 61; Pred. No.

DB 1; Length 886; 5.44e-01;

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Best Local S
Matches
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-I FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANS
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOI
MAKES DOUBLE-STRAND BREAKS.

-I CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND
OF DOUBLE-STRANDED DNA.

-I SUBUNIT: HOWODIMER (BY SIMILARITY).

-I SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.

-I SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.

-I EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NEGATI
POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX
NEGATIVE SUPERCOILS.

-I SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                           TP2B_MOUSE STAT

C6451;

15-JUL-1998 (REL. 3

15-JUL-1998 (REL. 3

15-DEC-1998 (REL. 3

DNA TOPOISOMERASE I

TOP2B.
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15-JUL-1998 (REL. 3
15-DEC-1998 (REL. 3
DNA TOPOISOMERASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-slb.ch).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TP2B_CRILO
Q64399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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"Cloning and characterization of full-length cDNAs coding for the DNA
topoisomerase II beta from Chinese hamster lung cells sensitive and
resistant 9-OH-eellipticine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00204; DNA_topoisoII; HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
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MEDLINE; 96085121
   MUS MUSCULUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                 922 IFVVDRNTVEI 932
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                                                                                                                                                                                                                                                                                                                                                                  IFVVDKNTGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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8; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOISOMERASE; DNA-BINDING; ATP-BINDING; NUCLEAR 814 814 DNA CLEAVAGE (BY SIMILARITY). 1612 AA; 182074 MW; AA9562E7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.1%;
larity 72.7%;
Conservative
(MOUSE)
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37,
11,
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37,
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
BETA ISOZYME (EC 5.99
                                                           CREATED)

LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)

BETA ISOZYME (EC 5.99.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61;
Pred. No.
2; Misma
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                                                                  (EC 5.99.1.3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UPDATE)
3 5.99.1.3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RELAX ONLY
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TOPOISOMERASE II
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RESULTANT OF THE PROPERTY OF T
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Best Local
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01-OCT-1993 (REL. 2
15-DEC-1998 (REL. 3
DNA TOPOISOMERASE I
                                                                                                                                                             MEDINE; 93087165.

JENKINS J.R., AYTON P., JONES T., DAVIES S.L., TAYTON P., JONES T., DAVIES S.L., THE STATE ALTON P., HICKSON I.D.;

"Isolation of cDNA clones encoding the beta isozyme of human topoisomerase II and localisation of the gene to chromosome 3 NUCLEIC ACIDS RES. 20:5587-5592(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOMERASE;
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIYAIKE M., ADACHI N., KIKUCHI A.;

SUBMITTED (SEP-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: CONTROL OF IOPOLOGICAL STATES OF DNA BY

-IE REAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS.

MAKES DOUBLE-STRAND BREAKS.

-I- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAG

OF DOUBLE-STRANDED DNA.
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RODENTIA; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00177; TOPOISOMERA; PF00204; DNA_topoisoII; HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                        SEQUENCE FROM N.A.
MEDLINE; 93192319.
AUSTIN C.A., SNG J.H., PATEL S., FISHER L.M.;
NOVEL HeLa topoisomerase II is the II beta isoform: cor
sequence and homology with other type II topoisomerases
BIOCHIM. BIOPHYS. ACTA 1172:283-291(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA;
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SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
NEGATIVE SUPERCOILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                           SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:98791; TOP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                       93087165.
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  얽
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                                                                                                                                                                                                                                                                                                                                                                                                                 CATARRHINI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOISOMERASE; DNA-BINDING; ATP-BINDING; NUCLEAR PROTEIN.
814 814 DNA CLEAVAGE (BY SIMILARITY).
1612 AA; 181863 MW; B496E4B5 CRC32;
  1038-1271
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ACHI N., KIKUCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26, CREATED)
27, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDAT
II, BETA ISOZYME (EC 5.99
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72.7%;
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Pred. No.
2; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    re 61; DB 1; Le
1. No. 5.44e-01;
Mismatches 1;
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MUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA;
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Best Local
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                               15-JUL-1998
15-JUL-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAVIES S.L., JENKINS J.R., HICKSON I.D.;
"Human cells express two differentially spliced topologyerase II beta mRMA.";
NUCLEIC ACIDS RES. 21:3719-3723(1993).
-!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF D.
-!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF D.
-!- BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRUBELE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE.
                                                               TP2B_CHICK
042131;
                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and characterization of a human novel DNA topoisomerase II homologue from FEBS LETT. 266:115-117(1990).
                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                        DNA
                                                                                                                                                                                                                                                                                          PFAM; PF00204; DNA_topoisoII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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AUSTIN C.A.,
  GALLUS
                                                                                                                                                                                                                                                          ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93376494.
           FOP2B
                                                                                                                                                                                                                                                                       HSSP; P06786; 1BGW.
ISOMERASE; TOPOISON
                                                                                                                                            934 IFVVDRNTVEI 944
                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                               L; X68060; G37231; -.
L; X71911; -; NOT_ANNOTATED_CDS.
L; Z15111; G288567; -.
L; Z15115; G288565; -.
L; X3662; G38325; -.
; S26730; S26730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: TWO FORMS, PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATED.
EUKARYOTIC TOPOISOMERASE I AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: NUCLEAR;
                      TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                      S26730;
S10710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSITIVE
                                                                                                                       IFVVDKNTGDI
 GALLUS
                                                                                                                                                                  Similarity 72.7%, 8; Conservative
                                                                                                                                                                                                                                                                                                     PS00177; TOPOISOMERASE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IS SHOWN HERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit
                                                                                                                                                                                                              1611
1626
                                                                                                                                                                                                                                                                     TOPOISOMERASE; DNA-BINDING; ATP-BINDING;
                               (REL.
                                                                                                                                                                                                                                               SPLICING; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUPERCOILS, WHEREAS SUPERCOILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISHER L.M.;
                                                                                                                                                                                                                                                                                                                              S41641.
(CHICKEN)
                                                                           STANDARD;
                                                                                                                                                                                                               AA; 183296 MW;
                  36, CREATED)
36, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDAT
II, BETA ISOZYME (EC 5.99
                                                                                                                                                                                                                          1611
                                                                                                                                                                             58.1%;
72.7%;
                                                                                                                                                                                                                                    826
28
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                                                                                                                                                                  Pred.
2; 1
                                                                                                                                                                                        Score
                                                                                                                                                                                                                      DNA CLEAVAGE (BY SIMILARITY).
MISSING (IN BETA-1).
T -> A (IN REF. 2).
                                                                                                                                                                                                              4191FFFD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROKARYOTIC
                                                                                                                                                                   Mismatches
                                                                                                                                                                                        61;
                                                                                                                                                                               Ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          II CAN RELAX BOTH ROKARYOTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOLUS
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OF THE
                                                                                                                                                                from HeLa cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               as its content
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TOP2B G
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                                                                                                                                                                                        Length 1626;
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GENE. THE B
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                     PHOSPHORYLATION;
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RELAX ONLY
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Matches
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01-NOV-1995 (REL. 3
01-NOV-1997 (REL. 3
HYPOTHETICAL 10.6 F
                                                                  SEQUENCE FROM N.A.
STRAIRS / MG1655;
MEDLINE: 812 97426617.
BLATTNER F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
GREGOR J., DAVIS N.W., KI
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; N
NEOGNATHAE;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (SEP-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOMERASE;
ACT_SITE
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            P46857;
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DOMAIN
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00204;
HSSP; P06786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB007446; D1023408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          +
                                            "The complete genome sequence of SCIENCE 277:1453-1474(1997).
                                                                                                                                                                            ESCHERICHIA COLI
BACTERIA; PROTEO
                                                                                                                                                                 SCHERICHIA.
                                                                                                                                                                                                                                                                                                                                   939 IFVVDRNTVEI
                                                                                                                                                                                                                                                                                                                          3 IFVVDKNTGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MI A., HARATA M., MIZUNO S.;
MITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DNA.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO TYPE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTIC TOPOISOMERASE I AN POSITIVE SUPERCOILS, WHEREAS NEGATIVE SUPERCOILS.
                                                                                                                                                                                                                                                                                      12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration -
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00177; TOPOISOMERASE_II; 1.
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1388
1393
1393
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                                                                                                                                                                                                                                                                           STANDARD;
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1391
1396
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72.7%;
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RMES; PHASIANIDAE; PHAS
                                                                                                                                                                                                             CREATED)
, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
PROTEIN IN GNTR-GGT INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                       183245
                                                                              T G. III, BLOCH C.A., PERNA N.T., S J., GLASNER F.D., RODE C.K., MA-KIRKPATRICK H.A., GOEDEN M.A., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-BINDING; ATP-BINDING;
DNA CLEAVAGE (BY SIMIL
POLY-GLY.
POLY-LYS.
                                                                                                                                                                             GAMMA SUBDIVISION;
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Pred.
2; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND II CAN RELAX BOTH AS PROKARYOTIC ENZYMES
                                                        Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       4EEAEAAB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                    81;
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                                                                                                                                                                                                                                                                                                                                                                                   DB 1; L
5.44e-01;
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PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                           94
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                                                                                                                                                                              ENTEROBACTERIACEAE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                               Length 1627;
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CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                             EMBL; U59325; G1389853; -. PROSITE; PS00232; CADHERIN; PRODUCTOR cadherin; 5.
                                REPEAT
CARBOHYD
                                                                                                                                   PROPEP
CHAIN
                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                              SHIBATA T., SHIMOYAMA Y., GOTOH M., HIROHABHI S., SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAROA; CHORDATA; VERTEBRATA; MAMMALIA;
DRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998
15-JUL-1998
15-JUL-1998
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                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL PROTEIN. SEQUENCE 94 AA; 10
                                                                                                                                                                     CALCIUM-BINDING;
                                                                                                                                                                                                                                                                                                                                                  MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CIL TYPES.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CADHERIN-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q13634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CADE_HUMAN
                                                       REPEAT
                                                                                       REPEAT
                                                                                                   DOMAIN
                                                                                                             TRANSMEM
                                                                                                                         DOMAIN
                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              fissue-brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 FIIDKDSGEIH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 45.5% es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 FVVDKNTGDIN 14
                                                                                                                                                                             ADHESION; GLYCOPROTEIN; PHOSPHORYLATION;
                                                                                                                                                                                        PF00028; cadherin; 5.
PF01049; Cadherin_C_term;
P15116; INCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U18997; G606381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE000421; G1789855; -.
NE; EG12948; YRHB.
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8 (REL. 36, 1
8 (REL. 36, 1
4 PRECURSOR.
160
269
255
455
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                     REPEAT;
57.1%;
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                                                                                                                                                                   SIGNAL
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Pred. No. 8.60e-01;
6; Mismatches 0;
        CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 5.
CADHERIN 5.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                 CYTOPLASMIC
                                                                                                            POTENTIAL
                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                CADHERIN-14
                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                (POTENTIAL).
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                                                                                                                                                                              TRANSMEMBRANE
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01-NOV-1997
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VARIANT
VARIANT
                                                                                                                               RNH2_HELPY
P56121;
                                                                                                                                                                                                                                                                                                                                                           EMBL; D14066; G222457; -.
PIR; JQ1917; JQ1917.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF00910; RNA_helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANOTATION UPDATE)
GENOME POLYPROTEIN [CONTAINS: 22.5 KD PROTEIN; 26 KD PROTEIN; 31 KD PROTEIN; PROBABLE RNA-DIRECTED RNA POLYPERASE (EC 2.7.7.48)].
PARSNIP YELLOW FLECK VIRUS (ISOLATE P-1.21) (PYFV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; SEQUIVIRIDAE;
SEQUENCE FROM N.A
STRAIN-26695 / ATO
                                   HELICOBACTER.
                                            HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION;
                                                                                   RIBONUCLEASE
                                                                                                                                                                                                                2246 FGVFGVNDTIGIIDV 2260
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                     POLYPROTEIN; ATP-BINDING; CO
RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright, It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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                                                                      RNHB OR HP1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93107855.
"The nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 93107855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  picorna-like virus.";
J. GEN. VIROL. 73:3203-3211(1992).
-!- SIMILARITY: SOME, TO THE CMPV AND TBRV POLYPROTEINS.
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(REL. 35,
(REL. 35,
 / ATCC 700392
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58.3%;
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LAST SEQUENCE UPDATE)
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3.1.26.4) (RNASE HII)
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4; Mismatc
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Pred. No. 8.60e-0
3; Mismatches
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                                              HELICOBACTER GROUP;
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Best Local Similarity 46.2%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000634; G2314491; -.
TIGR; HP1323; -.
HYDROLASE; NUCLEASE; ENDONUCLEASE; MAGNESIUM.
SEQUENCE 209 AA; 23176 MW; FA2B072C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the gastric pathogen Helicobacter pylori.";
NATURE 388:539-547(1997).
-I- FUNCTION: DEGRADES THE RIBONUCLEOTIDE MOIETY ON RNA-DNA HYBRID MOLECULES (BY SIMILARITY).
-I- CATALLYIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 5'-PHOSPHO-
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TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
BERG D.E., GOCAYME J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MONOESTER.
-!- SIMILARITY: WITH OTHER RNASE H FROM BACTERIA, FUNGI, AND WITH RNASE H DOMAINS FROM POL OF RETROVIRUSES.
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67 GFFVVKKSANEID 79
|:||| |::::|:
2 GIFVVDKNTGDIN 14
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Search completed: Fri Jun 11 17:16:12 1999 Job time: 8 secs.

"我有非常会会有这些感染的有有有的的,我们也有有的的,我们就是我们的,我们的人们的,我们的人们的,我们的人们的人们的人们的人,我们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人们的人	[] [] [] [] [] [] [] [] [] [] [] [] [] [

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:16:29 1999; MasPar time 6.21 Seconds 131.825 Million cell updates/sec

Tabular output not generated...

Description: Perfect Score: Sequence: Title: >US-08-991-628-2 (1-15) from US08991628.pep

1 FGIFVVDKNTGDINI 15

Scoring table: PAM 150 Gap 15

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 26.631; Variance 35.345; scale 0.753

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

66 62.9 78 13 66 62.9 1329 66 57.1 3380 5 60 57.1 598 1 59 56.2 154 1 59 56.2 245 1 59 56.2 1033 2 58 55.2 1033 1 58 55.2 270 1 58 55.2 816 1 58 55.2 950 13 58 55.2 1035 13 58 55.2 1035 13 58 55.2 1036 1 58 55.2 1036	85.7 993	Query Score Match Length I
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CHICKEN CADHERIN-7. C45G7.6 PROTEIN. ADHERIN. HYPOTHETICAL 24.5 KD P ALDEHYDE FERREDOXIN OX HYPOTHETICAL PROTEIN M HYPOTHETICAL PROTEIN M HYPOTHETICAL PROTEIN M PV72. PILC PROTEIN. CONSERVED HYPOTHETICAL HYPOTHETICAL 68.6 KD P KIAA0345-LIKE 9 PARAXIAL PROTOCADHERIN NF-PROTOCADHERIN NF-PROTOCADHERIN PCDH7 (BH-PCDH)A. PCDH7 (BH-PCDH)C. 504AA LONG HYPOTHETICA	DESMOGLEIN 3 (FRAGMENT	Description
1.08e-01 1.10e+00 1.72e+00 1.72e+00 2.68e+00 2.68e+00 2.68e+00 4.15e+00	4.88e-07	Pred. No.

21 57 54.3 792 13 093319 CADHERN 11. 22 57 54.3 794 13 093264 CADHERIN PRECURSOR. 23 57 54.3 797 11 Q63418 PROTOCADHERIN 3. 24 57 54.3 798 2 Q50288 PUTATIVE LIPOPROTEIN. 25 57 54.3 810 4 075281 KIAAQ345-LIKE 8. 26 57 54.3 814 4 075281 KIAAQ345-LIKE 8. 26 57 54.3 814 4 075281 CENTRIN 1 (FRAGMENT). 27 56 53.3 171 5 061171 CENTRIN 1 (FRAGMENT). 28 56 53.3 423 10 065875 CELL DIVISION PROTEIN. 29 56 53.3 601 2 086691 PUTATIVE TRANSPORT SYS 30 56 53.3 831 5 P91388 COMMID K1ZD9. 31 55 52.4 112 1 Q58642 HYPOTHETICAL 16.3 KD p 32 55 52.4 261 13 042389 SUCRASE-ISOMALTASE (FR 36 55 52.4 261 13 042389 SUCRASE-ISOMALTASE (FR 36 55 52.4 437 10 022170 FRASTUR WOCLEOTIDE SU 39 55 52.4 437 10 022171 POLYMERASE (FRAGMENT). 39 55 52.4 437 10 022171 POLYMERASE (FRAGMENT). 39 55 52.4 1194 2 045916 138KDA PROTEIN ASSOCIA 40 55 52.4 1196 2 033550 PROGENTIOR TOOL OLOON 41 55 52.4 1196 2 033550 PROGENTIOR SUCRIN I NON 45 52.4 1196 9 038197 READTHROUGH STOP CODON 45 55 52.4 1616 14 P89676 183K PROTEIN.	4 4 5 4	- 4-	_																					
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ALIGNMENTS

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RESULT RE
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  Query Match
Best Local S
Matches
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    076356 PREL:
076356; CTRE:
01-NOV-1998 (TRE:
01-NOV-1998 (TRE:
01-NOV-1998 (TRE:
C15G7.6 PROTEIN.
C45G7.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subpopulation-specific expression controlled by sequential and DEVELOPMENT 121:1321-1332(1995).

-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; D42150; D1008306; -.
PROSITE; PS00232; CADHERIN; 3.
PPAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin; 5.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT SEQUENCE 785 AA; 87171 MW; F27A6881 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARREILLE P.,
LIGHTNING J., LLOYID C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPEA, SUUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WARTSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                             SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE
EMBL; AF067511; G3193145; --
PROSITE; PS00232; CADHERIN; 1.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE
SEQUENCE 1329 AA; 146518 MW; B161D39E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "2.2 Mb of contiguous nucleotide sequence from
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
DANTE M., WAMSLEY P.;
"The sequence of C. e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                     SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SIKAIN-WHITE LEGHORN; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95309115.
NAKAGAWA S., TAKEICHI M
Neural crest cell-cell
     Local Similarity
nes 8; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
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                                                                                                                                                                                                                                                                                                                                                  (3UN-1998)
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                               elegans cosmid C45G7."; ) TO EMBL/GENBANK/DDBJ D
                         60.0%;
72.7%;
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Pred. No.
4; Misma
Score
Pred.
2; M
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                               TRANSMEMBRANE; CALCIUM-BINDING; W; B161D39E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
  Mismatches
                         N 63;
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                                              DB 5;
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                                                                                                                                                                                            DATA BANKS.
PROTEIN (BY
                                                                                                                                                                                                                                                                                                                                               DATA BANKS
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Indels
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Best Local S
Matches
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-PCC6803;
MIDLINE; 97661201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKA
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMOTO S., KIMURA
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAWOTO S., KIMURA
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996
01-NOV-1996
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Q55701;
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EUKARYOTA;
PTERYGOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADHERIN.
DACHSOUS.
                                                                                                                                                                                                                                                                                          MEDLINE; 96127529.

KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N., SUGLURA M., TARATA S.,

"Sequence analysis of the genome of the unicellular cyanobacterium "Synechocystis sp. strain PCC6803. I. sequence features in the 1Mb region from map positions 64% to 92% of the genome.";

DNA RES. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00028; cadherin; 26.
CELL ADHESION; GLYCOPROTEIN;
SEQUENCE 3380 AA; 366356 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLYBASE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL 24.5 KD PROTEIN
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CLARK H.F., BRENTRUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     imaginal disc morphogenesis
GENES DEV. 9:1530-1542(1995)
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PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYANOBACTERIA;
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METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSE
DIFTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TREMBLREL.
(TREMBLREL.
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larity 58.3%;
Conservative
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er of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROOCOCCALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE I MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HNEIT2 K., BIEBER A., GOODMAN C., of the cadherin superfamily that in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST
LAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
4; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TRANSMEMBRANE; MW; 7D83FAC3 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
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ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN
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                                                                                                                                   NAKAMURA
                                         URA T.,
K., OKUMURA S.,
YASUDA M.,
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PRESCRIPTION OF REAL PROPERTY OF THE PROPERTY 
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Best Local
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Best Local Similarity 42.9%;
Matches '6; Conservative
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                                                                                                                                                                                          Q58735
Q58735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLERK H.-P., CLAYTON.R.A., TOMB J.-F., WHITE O., NELSON K.E., KICCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S. KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZH OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
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029907
029907;
METHANOCOCCUS JANNASCHII
ARCHAEA; EURYARCHAEOTA; N
METHANOCOCCUS.
                                                                                          01-JUN-1998 (TREMBLREL 06, 01-JUN-1998 (TREMBLREL 06, 01-JUN-1998 (TREMBLREL 06, HYPOTHETICAL PROTEIN MJ1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROPERTY S98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001081; G2650295;
TIGR; AF0340; -.
PFAM; PF01314; AFOR; 1.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sulphate-reducing archaeon Archaeoglobus NATURE 390:364-370(1997).
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MEDLINE; 9804
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01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                         HYPOTHETICAL MJ1339.
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-VOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ALDEHYDE FERREDOXIN OXIDOREDUCTASE (AOR-3).
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                                                                                                                                                                                                                                                                                                                                                                     355
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                                                                                                                                                                                                                                                                                                                                                                                                                Match 57.1%;
Local Similarity 40.0%;
les 6; Conservative
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98049343.
                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                369
                    METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 60; D
Pred. No. 1:
6; Mismatc
                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.72e+00;
7; Mismatches 1
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1.72e+00;
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Best Local S
Matches
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Best Local :
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                      048662;
048662;
01-JUN-1998
01-JUN-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998
01-JUN-1998
01-JUN-1998
                                                                                                                                  151 YGIFVVDK 158
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1 FGIFVVDK 8
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Q58723
Q58723;
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BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.F., BORODOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCIENCE 273:1058-1073(1996).
EMBL; U67574; G1591981; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                              EMBL; U67573;
HYPOTHETICAL
                                                                                                                                                                                                                                                                        SCIENCE 273:1058-1073(1996).
EMBL; U67573; G1591968; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHANOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHANOCOCCUS JANNASCHII.
ARCHAEA; EURYARCHAEOTA; N
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                                                                                                                                                                                                         Similarity
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Similarity 42.9%;
6; Conservative
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245 AA; 2
                      (TREMBLREL.) (TREMBLREL.)
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3 (TREMBLREL. 06,
3 (TREMBLREL. 06,
11 PROTEIN MJ1327.
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                                                                             PRELIMINARY;
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                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                       56.2%;
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                                                                                                                                                                                       Score 59;
Pred. No.
1; Misma
                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.68e+00;
4; Mismatches 4
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CUCURBITA

MAXIMA

(PUMPKIN)

(WINTER

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Best Local
Matches
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Best Loc
Matches
SEQUENCE FROM N.B.

STRALN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE; 98049343.

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

KETCHUM K.A., DODSON R.J., LEE N.H., SUTTON G.G., GILL S.,

FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

FLEISCHMANN R.D., GUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

FLEISCHMANN R.D., GUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

FLEISCHMANN R.D., GUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

FLEISCHMANN R.D., GUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O33373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998
01-JAN-1998
01-AUG-1998
                                                                                                                                                                                                                                       028514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHIMADA T., KUROYANAGI M., NISHIMURA M., HARA-NISHIMURA I.;
"A pumpkin 72-kDa membrane protein of precursor-accumulating
"a characteristics of a vacuolar sorting receptor.";
PLANT CELL PHYSIOL. 38:1414-1420(1997).

EMBL; AB006809; D1026005; -.
EMBL; AB006809; D1026005; -.
PROSITE: PS00110; ASX_HYDROXYL; 1.
PROSITE: PS01187; EGF_CA; 1.
GLYCOPROTEIN; EGF-LIKE DOMAIN.
SEQUENCE 624 AA; 69028 MW; AAA97DOB CRC32;
                                                                                                                                                                          CONSERVED AF1760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEISSERIA
BACTERIA;
                                                                                                                                                                                   01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
CONSERVED HYPOTHETICAL E
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TISSUE-DEVELOPING COTYLEDON;
MEDLINE; 98182943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; VIRI EUPHYLLOPHYTES;
                                                                                                                                                                                                                                                                                                                                                                                                           BARCKMAN M., KAELLSTROEM H., JO:
MICROBIOLOGY 144:149-156(1998).
EMBL: AJ001121; E334755; -.
SEQUENCE 1033 AA; 112936 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-GC-653;
                                                                                                                                              ARCHAEOGLOBUS FULGIDUS. ARCHAEA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUCURBITALES;
                                                                                                                                     ARCHAEOGLOBUS.
                                                                                                                                                                                                                                                                                                                                 804 YGIFDDDKGTGTVKV 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QUENCE FROM N.A.
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Local
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                                                                                                                                                                                                                                                                                                                                                        h 56.2%;
Similarity 46.7%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 70.0% 7; Conservative
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PROTEOBACTERIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TREMBLREL.
(TREMBLREL.
                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPERMATOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.2%;
                                                                                                                                                                                   . 05, CREATED)
. 05, LAST SEQUENCE UPDATE)
. 07, LAST ANNOTATION UPDAT
PROTEIN.
                                                                                                                                                ARCHAEOGLOBALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05,
07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; HYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA SUBDIVISION; NEISSERIACEAE;
                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
4; M
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred.
2; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 JONSSON A.B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1033
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2.68e+00;
                                                                                                                                                                                                                                                    270
                                                                                                                                                                                                                                                                                                                                                                     DB 2; L
2.68e+00;
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                                                                                                                                                ARCHAEOGLOBACEAE;
                                                                                                                                                                                                                                                                                                                                                          4;
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Best Local
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SEQUENCE FROM N.A. KIMMERLY W., BONDOC M., CH KADNER K., MIGUEL T., MILL SUBRAMANIAN S., MARTIN C.H "Sequencing of human chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7LT 12
065522
065522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD I.K., UTTER. COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M. SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A. MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R. VENTER J.C.;
                                                                                                                                                                                                                                                                                               EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ
EMBL; AL022537; E1287270;
HYPOTHETICAL PROTEIN.
SEQUENCE 593 AA; 68632 MW; 9EA10B88 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence sulphate-reducing archaeon Arc NATURE 390:364-370(1997).
EMBL; AE000981; G2648791; -.
TIGR; AF1760; -
                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                               01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                            075284
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

BEVAN M., BENES V., RECHMANN S., BORKOVA D
MEWES H.W., MAYER K.F.X., SCHUELLER C.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                     ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARXOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL
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                                                                                                      KIAA0345-LIKE
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Similarity 40.0%;
6; Conservative
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(TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
L 68.6 KD PROTEIN.
                                                                                                                                                                                                                                                   55.2%;
larity 35.7%;
Conservative
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                                                                                                                                                                                                                                541
             M., CHENG J.,
, MILLER C., I
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                                                                                                                                                                                                                                                    Score 58;
Pred. No.
7; Misma
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Pred.
5; }
                                                                                                               CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
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                                                                                VERTEBRATA;
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                 9EA10B88 CRC32;
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                      PITLUCK S., POLLARD M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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No. 4.15e+00;
                                                                                                                                                              816
                                                                                                                                                                                                                                                 DB 10; 4.15e+00; 2;
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                                                                                                               ON UPDATE)
                                                                                                                                                                                                                                                                                                                                    DATA
                                                                                MAMMALIA;
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                                                                                EUTHERIA;
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                       ROJESKI
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Best Local S
Matches
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Best Local'Similarity 41.7%;
 Query Match
Best Local Similarity
Matches 7; Conser
                                                        SEQUENCE FROM N.A.

BRADLEY R.S., ESPESETH A., KINTNER C.;

CURR. BIOL. 0:0-0(1298).

11- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; AF043643; G2852363; -..

PROSITE: PRO0232; CADHERIN; 6.

PROSITE: PRO10232; CADHERIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAC CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAC SEQUENCE 1035 AA; 113713 MW; 7E4D3C4E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

DE ROBERTIS E.M.;

YAMAMOTO A., DE ROBERTIS E.M.;

SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; AF042191; G3201662; -.

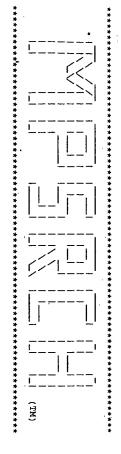
PROSITE; PS00232; CADHERIN; 5.

CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT.

CELL ADHESION; GLYCOPROTEIN; 96B102F0 CRC32;
                                                                                                                                                                                                                                                                                                                                                    057537;
057537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System.";
SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC005609; G3540165; -.
                                                                                                                                                                                                                  XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                               01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEDOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; RASBORINAE; DANIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TREMBLREL 08, CREATED)
01-NOV-1998 (TREMBLREL 08, LAST SEQ
01-NOV-1998 (TREMBLREL 08, LAST ANN
PARAXIAL PROTOCADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (SEP-1998)
                                                                                                                                                                                                                                                                                     NF-PROTOCADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     615 LFSIDKNTGEI 625
:| :||||:|
3 IFVVDKNTGDI 13
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| ::: |||:|::
| 4 FVVDKNTGDINI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RICKE D.O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 55.2%;
Local Similarity 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 AA;
   55.2%;
ilarity 50.0%;
Conservative
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Score 58; DB 13; Length 1035; Pred. No. 4.15e+00; 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB 4; I
Pred. No. 4.15e+00;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 13; Le
Pred. No. 4.15e+00;
3; Mismatches 1;
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                                                                                REPEAT
 Gaps
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Db 552 GIFSIHPDTGDITV 565
|||::|||:
Qy 2 GIFVVDKNTGDINI 15
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Search completed: Fri Jun 11 17:18:36 1999 Job time: 127 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:27:18 1999; MasPar time 4.80 Seconds 66.422 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-3
Description: (1-15) from US08991628.pep
Perfect Score: 96

uence: 1 LNSKIAFKIVSQEPA 15

Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

statistics: Mean 18.085; Variance 51.973; scale 0.348

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	₽B	Ħ	Description	Pred. No.
- :	96	100.0	15	35	W78814	Desmoglein 3 protein	3.65e-04
N	96	100.0	15	20	W04843	ě	3.65e-04
ω	96	100.0	15	ω	W64815		3.65e-04
4	96	100.0	614	19	W07908	Pemphigus vulgaris an	3.65e-04
U	96		999	σ	R30742	Human pemphigus vulga	3.65e-04
o	87	90.6	778	21	W15489	Pemphigus foliaceus a	5.06e-03
7	77	80.2	263	24	W13010	Segment of desmosomal	8.83e-02
œ	77	80.2	560	24	W13009	Segment of desmosomal	8.83e-02
9	54	56.3	878	10	R55060	Sequence of human liv	4.45e+01
10	54	56.3	878	15	R85487	Human E-cadherin prec	4.45e+01
11	54	56.3	2233	ű	W48711	HPIV-3 JS isolate wil	4.45e+01
12	54	56.3	2233	$\mathfrak{S}_{\mathfrak{S}}$	W48712	HPIV-3 FRhl cp45 vacc	4.45e+01
13	54	56.3	2233	33	W48713	HPIV-3 Vero cp45 vacc	4.45e+01
14	53	55.2	456	37	W82841	Human cerebral protei	5.74e+01
15	49	51.0	572	œ	R40843	Bilirubin oxidase.	1.57e+02
16	49	51.0	916	21	W13129	Full length human cad	1.57e+02

45	44	43	42	41	40	39	3 8	37	36	<u>ω</u>	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18
46	46	46	46	46	46	46	46	46	46	46	46	46	47	47	47	47	47	47	47	47	47	48	48	48	48	48	49
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8	5	51	R99579	22	4	85	W34554	20	5	63	62	3	24	~	73	73	R75741	88	74	8	2	28	91	W23994	9	19	R24307
-	Mouse multidrug resis	P.denitrificans COB N	arge subuni	onal prote	Yeast RNA-binding pro	Desulfurococcus MIITL	MllTL glycosidase 29G	T-C	T-cell	Human SLAM3 T-cell co	Human SLAM2 T-cell co	cus	Virulence gene cluste	PPI.	urgdorferi	B. burgdorferi strain	outer surfa	Human secreted protei	Staphylococcus aureus	Human secreted protei	Mamalian growth hormo	Cardiac sodium channe	sodium	Human hH1 sodium chan	H. pylori inner membr	Bacteriophage spol Po	Translation of ORF 3
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ALIGNMENTS

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into phagocytic cells. treating genetic diseas an immune response.

diseases,

infections or

can be used for gene therapy, e.g. for infections or tumours or for downregulating

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Transcorring and disease

Transcorring and separations for tolerisation to antigens comprise Claim 1; Page 39; 58pp; English.

Ce Pharmaceutical preparations for tolerisation to antigens comprise CC either an isolated human non-collagen or non-myslin basic protein CC (MBP) polypeptide which is capable of tolerising an individual to an CC autoantigen; or an isolated human pathogen polypeptide capable of CC tolerising an individual to that polypeptide. In both cases, the CC polypeptide (whether self or non-self) includes an amino acid CC sequence corresponding to a sequence motif for a MHC class II CC protein, such as HLA-DR, which is associated with a human autorimune CC disease and which binds to the polypeptide to activate autoreactive CC -cells in individuals with the autoimmune disease. This peptide is CC derived from the human desmoglein 3 protein (amino acids 190-204) CC and is implicated as a self epitope in pemphigus vulgaris. Peptides of derived from the human desmoglein protein are described in w04841-47.
RESULT
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Self epitope of desmoglein 3, implicated in autoimmune disease.
Tolerisation; self-epitope; antigen; autoimmune disease;
autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;
pemphigus vulgaris; desmoglein; multiple sclerosis;
herpes simplex virus; adenovirus; phosphomannomutase;
human papillomavirus; Epstein-Barr virus; DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W04843;
W04843;
                                                                                                                                  W64815
W64815
                             US5783567-A.
                                                           29'SEP-1998 (first entry)
Desmoglein-3 190-204.
Desmoglein, DG; gene therapy; pemphigus vulgaris;
autoantigen; autoimmune disease; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strominger JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1995; US-400796.
(HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-1996; U03182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9627387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nfluenza; haemagglutinin; reovirus; sigma protein
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Similarity 100.0%;
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Similarity 100.0%;
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Pred. No.
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No. 3.65e-04;
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Best Local Similarity 100.0%;
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30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgG1 hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microparticle encapsulated nucleic acids expression of proteins e.g. in gene therapy Disclosure; Column 4; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curley JM, Hedley ML, Langer WPI; 98-427077/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pemphigus vulgaris antigen protein extracellular region. Autoantibody; immunoglobulin G; IgGl; fusion protein; ditreatment; pemphigus vulgaris; PV; bulla; blister; skin
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                                                                                                                                   pemphigus vulgaris.
Sequence 614 AA;
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Similarity 100.0%;
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d. No. 3.65e-04;
Mismatches 0;
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No. 3.65e-04;
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in disease;
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27-NOV-1991; 1
(USSH) US DE
Amagai M, Kl
                                                                   foliaceus patient autoantibody which comprises the constant region of 19G linked to the extracellular region of pemphigus foliaceus antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion protein is immobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful in immonodiagnosis. The fusion protein has little or no side effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding pemphigus vulgaris antigen diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English. This sequence is the pemphigus vulgaris and its encoding DNA may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                        Pemphigus foliaceus antigen-IgG constant region fusion p
Pemphigus foliaceus; autoantibody; constant region; IgG;
extracellular region; antigen; hinge portion; skin;
dermatitis herpetiformis; fusion protein; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pemphigus vulgaris. It is thought that the antigen may adhesion molecule.
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                                                                                                                                                                                                           Pemphigus foliaceus antigen-IgO constant region fusion protein through the hinge region used to treat pemphigus foliaceus Claim 1; Page 10-12; 17pp; Japanese. This sequence represents a fused protein recognised by pemphigus
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15-DEC-1992.
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Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
                                                                                                                                                                                                                                                                         P-PSDB; T66428
                                                                                                                                                                                                                                                                                    (NISH/) NISHIKAWA T. WPI; 97-241758/22.
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25-MAR-1997.
12-SEP-1995; 260899.
12-SEP-1995; JP-260899.
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                                                         immunodiagnosis.
Juence 778 AA;
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NOV-1991; US-798918.
SH) US DEPT HEALTH & H
gai M, Klaus-kovtun V,
; 93-067436/08.
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Similarity 100.0%;
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    Conservative
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V, Stanley JR;
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2; Mismatc)
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Pred. No. 3.65e-04;
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RESULT
1 W13010; standard; protein; 26 AC W13010; standard; protein; 26 AC W13010; Segment of desmosomal cadherin; desmost carcinoma; desmosome; antibo micrometastasis; separation; KW carcinoma; desmosome; antibo micrometastasis; separation; KW metastatic.
OS Homo sapiens.
PN D27-FEB-1997.
PF 3-AUG-1995; D5-031033.
PA (PROG-) PROGEN BIOTECHNIK GM Franke WW, Schaefer S; DR WFI; 97-146518/14.
PT surface of epithelial or car useful for diagnosis and tree ps Claim 9; Page 5; 8pp; German CC The present sequence is a sec CC diagnose, i.e. to detect car discrometastases, not bound to detect living or fixed carcinoma; and ce carcinoma; and the carcinoma calls and not detect as a therapeutic to deliver target cells. The Ab provide CC metastatic carcinoma, and de carcessible in desmosome boun CC carcinoma.
SQ Sequence 263 AA;
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23-AUG-1995; 031033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaefer S;
WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a segment of the desmosomal cadherin (D desmoylein Dsy2, which is exposed on the surface of epithelial carcinoma cells and not bound to desmosomes. An antibody (Ab) directed against epitopes of the present sequence can be used to diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes, to separate, enrich o detect living or fixed carcinoma cells by cell sorting methods as a therapeutic to deliver agents, e.g. other Ab or toxins, to target cells. The Ab provides rapid and reliable detection of metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes useful for diagnosis and treatment of carcinoma micrometastases claim 7; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab)
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23-AUG-1995; D31033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaefer S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosom useful for diagnosis and treatment of carcinoma micrometastases Claim 9; Page 5; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Segment of desmosomal cadherin, desmoglein Dsg2.

Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithe carcinoma; desmosome; antibody; epitope; diagnosis; detectio micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 8
W13009 standard; protein;
                                                                                                                                                                           WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                             Homo sapiens.
DE19531033-A1.
                                                                                                                                                                                                                                                                                                                                                           metastatic.
                                                                                                                                                                                                                                                                                                                                                                             micrometastasis;
                                                                                                                                                                                                                                                                                                                                                                                                      carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                           Desmosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                Segment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 lnskisyrivslepa
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                                                                                                                                                                                                                                                                                                                                                                         desmosomal cadherin, desmoglein Dsg2.
cadherin; desmoglein; Dsg2; cell; surface; epithe
desmosome; antibody; epitope; diagnosis; detectic
desmosome; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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  epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560
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Pred. No. 8.
3; Mismatc
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present
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8.83e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface; epithelial;
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RESULT
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                                                                                                                                                                                                                          ş
                                                                                                                                                                                                                                                                         문
                                                                                                                                                                                                                                                                                                                                                                                                 Pri Purified human E-cadherin protein and nucleic acid - used to prodevelop prods. for diagnosis, prognosis, therapy and prophylaxis pr of t-cadherin disorders, e.g. malignancies

Pri of t-cadherin disorders, that is also known as sobtd.

CC by screening normal human liver and hepatocellular carcinoma cDNA

CC takes 402-513; AAS 178-513; AAS 178-189; AAS 178-289; AAS 290-274; AAS 402-513; AAS 178-513; AAS 151-703; AAS 178-289; AAS 28-878; CC 2749; 566-2749; 1-1053; 510-2596; 1332-3000; 540-1500; 348-906; 890-2016, 891-1053; 510-2596; 1332-3000; 540-1500; 348-906; 890-2016, 891-1053; 510-2596; 1332-3000; 540-1500; 348-906; 890-2016, 891-1053; 510-2596; 1332-3000; 540-1500; 348-906; 890-2016, 891-1053; 510-2596; 1332-3000; 540-1500; 348-906; 890-2016, 891-1053; 510-2596; 1332-3000; 540-1500; 348-906; 890-2016, 891-204; 2459-2775; DNA encoding at least 30 AAS selected from catherin cathe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
best Local S
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Best Local
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                     Human E-cadherin precursor.
E-cadherin; T-lymphocyte; alpha-E,beta-7 integrin;
auto1mmune disease; Crohn disease; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1994.
16-NOV-1993; U11097.
17-NOV-1992; US-978897.
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                                                                                                                                 T 10
R85487 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYYA ) UNIV YALE.
Morrow JS, Rimm DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnose, i.e.
                                                                                      18-MAR-1996
                                                                                                                R85487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equence of
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                                                                                                                                                                                                                                                                    293 naaiaytilsqdp 305
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                                                                                                                                                                                                                                                                                                        56.3%;
Local Similarity 53.8%;
les 7; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LNSKIAFKIVSQEPA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human liver E-cadherin.
human liver E-cadherin; cell adhesion molecule;
elial-cadherin; E-cadherin; cell adhesion molecule;
r.-CAM: Cell CAM 120/80.
                                                                                      (first entry)
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73.3%;
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Pred.
                                                                                                                                                                                                                                                                                                                 Score 54; DB 10; Le
Pred. No. 4.45e+01;
4; Mismatches 2;
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No. 8.83e-02;
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Best Local
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                                                                                                                                                                                                                                                       02-APR-1998.
19-SEP-1997, U16718.
27-SEP-1996, US-026823.
(AMCY) AMERICAN CYANAMID CO.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Murphy BR, Randolph VB, Sidhu MS, Tatem JM
WPI; 98-230710/20.
N-PSDB; V18272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page. 70-75; 103pp; English.

The human E-cadherin protein precursor (R85487) is expressed by an cDNA clone (T05764) derived from human liver. The extracellular ancount of E-cadherin is used to generate peptides that specifically bind to heterotypic cognates of E-cadherin and which inhibit adhesion of intra-epithelial T-lymphocytes to E-cadherin-expressing epithelial or endothelial cells in vitro or in vivo, thereby modulating mucosal immune responses. Such peptides are also specifically reactive with a monoclonal antibody (E4.6 or E6.1) that binds to E-cadherin and that can inhibit T-cell binding.
                                                             Recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus pisclosure; Page 246-254; 426pp; English.

This sequence represents the wild-type L protein from Human parainfluenza virus (HPIV-3) type 3 isolate JS. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, the protein from the sequence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting adhesion of T lisolating agents to treat psoriasis, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BGHM ) BRIGHAM & WOMENS Brenner MB, Cepek KL; WPI; 95-392921/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
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                 involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order mononegavirales which have at least 1 attenuating mutation in the 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPIV-3 JS isolate wild-type L protein.
L protein; attenuation; non-segmented; negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T05764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-1994; US-237919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human parainfluenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W48711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ingle stranded RNA virus; Mononegavirales
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     larity 53.8%;
Conservative
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151..702
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727..876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphocytes with E-cadherin auto-immune diseases e.g. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 15; L4
Pred. No. 4.45e+01;
4; Mismatches 2;
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mutation in the RNA
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ohn's disease,
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Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                    HPIV-3 Vero cp45 vaccine L protein.
L protein: attenuation; non-segmented; negative sense; single stranded RNA virus; Mononegavirales.
Human parainfluenza virus.
W09813501-A2.
02-APR-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M48713 standard; P
W48713;
W48713;
13-OCT-1998 (firs
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27-SEP-1996; US-026823.
(AMCY) AMERICAN CYLNAMID CO.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
MUIPHY BR, Randolph VB, Sidhu MS, Tatem
WPI; 98-230710/20.
                                                                                                                03-APR-1998.
19-SEP-1997; U16718.
27-SEP-1996; US-026823.
(AMCY) AMERICAN CYANAMID CO.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
MUTPHY BR, RANDOLPH VB, SIDHU MS, Tatem
WPI; 98-230710/20.
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This sequence represents the Human parainfluenza virus (HPIV-3) type 3 vaccine FRhl cp45 I protein. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI genomic promoter region and at least 1 attenuating mutation in the RNI polymerase gene. This RNA virus can be used as a vaccine to immunise a content of the promoter region and at least 1 attenuating mutation in the RNI polymerase gene. This action is the promoter region and at least 1 attenuating mutation in the RNI polymerase gene. This action is the promoter region and at least 1 attenuating mutation in the RNI polymerase gene. This action is the promoter region and at least 1 attenuating mutation in the RNI polymerase gene.
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N-PSDB; V18273\.
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                                                                                N-PSDB; V18274
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ingle stranded RNA virus; Mononegavirales.
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PT polymerase gene, useful as vaccine to immunise against such virus PS Disclosure; Page 283-291; 426pp; English.

CC This sequence represents the Human parainfluenza virus (HPIV-3) type 3 CC vaccine Vero cp45 L protein. This sequence is used in a method which CC involves the isolation of recombinantly-generated, attenuated, CC non-segmented, negative-sense, single stranded RNA virus of the order CC Mononegavirales which have at least 1 attenuating mutation in the 3' CC genomic promoter region and at least 1 attenuating mutation in the RNA CC polymerase gene. This RNA virus can be used as a vaccine to immunise an CC individual against such a virus.
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J05199882-A.
10-AUG-1993.
24-JAN-1992;
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The present sequence represents human cerebral protein-1 (HUCEP-1 has neuron function activating activity. HUCEP-1 is ufor treating ischaemic brain diseases and nerve denaturation conditions such as Parkinson's and Alzheimer's diseases. Sequence 456 AA;
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19-MAR-1997; 065716.
19-MAR-1997; JP-065716.
                                                                                                                                                                                                               Bilirubin oxidase.
Bilirubin; oxidase; analytical;
polymerase chain reaction.
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24-FEB-1994 (first entry)
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WPI; 98-575902/49.
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39..534
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l. No. 5.74e+
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No. 4.45e+01;
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5.74e+01;
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PR 24-JAN-1992; JP-034126.

PA (AMAN) AMANO PHARM KK.

DR WPI; 93-284681/36.

DR N-PSDB; Q47790.

PT Bilirubin oxidase prepn. useful as an analytical enzyme - by culturing bilirubin oxidase in transformant culture

PS Claim 1; Page 29-32; 32pp; Japanesse.

CC The sequence encodes bilirubin oxidase. The protein produced has a cc 38 amino acid signal peptide which is removed to give the mature cc protein (R40843).

SQ Sequence 572 AA;

Ouery Match

Best Local Similarity 13.3%; Pred. No. 1.57e+02;

Matches 2; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Matches 2; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

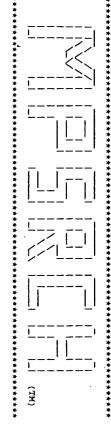
Db 282 idtrlpfkviasdsg 296

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Qy 1 LNSKIAFKIVSQEPA 15

Search completed: Fri Jun 11 17:29:04 1999

Job time: 106 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:25:31 1999; MasPar time 4.28 Seconds 140.445 Million cell updates/sec

Title: >US-08-991-628-3
Description: (1-15) from US08991628.pep
Perfect Score: 96
Sequence: 1 LNSKIAFKIVSQEPA 15

Scoring table: PAM 150 Gap 15

122810 segs, 40068593 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

י אייאסר אי שמוווויסרו.

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 25.594; Variance 33.108;

scale 0.773

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative

Score 96; DB 1; Length 999; Pred. No. 2.05e-09; 0; Mismatches 0; Indels

0

Gaps

0,

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•		51.0	•	•	52.1	52.1	52.1	52.1	•	52.1	52.1	52.1	52.1	53.1		53.1			•	•	54.2
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5.75e+01	٠	5.75e+01	3.81e+01	3.81e+01	3.81e+01	3.81e+01	٠	3.81e+01		3.81e+01		3.81e+0	3.81e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01	1.65e+01	1.65e+01

ALIGNMENTS

SUMMARY	937-966 110,180,545	616-639 640-999	496-598	270-383	52-157	יים אינו מטיים אינו	24+49	FEATURE		KEYWORDS	#map_position CLASSIFICATION	##cross-references	#qene	GENETICS	##Cross-references	##molecule	#accession	#cross-refere	#title	#journal	REFERENCE	ACCESSIONS		TITLE ALTERNATE NAMES	RESULT 1
#length 999 #molecular-weight 107502 #checksum 8311	#domain desmoglein repeat #label DG2\ #binding_site carbohydrate (Asn) (covalent) #status		cadherin repeat homology #label CR5\	cadherin repeat homology #label	cadherin repeat homology	c desimostern momoros * status predicted *	#domain propeptide #status predicted #label PRO\	#domain signal sequence #status predicted #label SIGV	transmembrane protein		; 18q12.1–18q12.2 #superfamily cadherin; cadherin repeat homology	ferences GDB:134030; OMIM:169615	GDB: DSG3		GB:M76482;	##TOSIGNOS 1-999 ##]abol AMA	A41088	pemphigus vulgaris, a disease of cell adhesion. #cross-references MUID:92069753	a novel	Cell (1991) 67:869-877	•	18-Sep-1998 A41088	#formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change	desmoglein 3 precursor - human pembhigus vulgaris antigen	IJHUG3 #type complete

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#gene
CLASSIFICATION
KEYWORDS
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**cross-references GB:S64268; GB:S64270

REFERENCE A37785
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#cross-references MUID:92037656
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##residues 44-1001,'AQPPSAT' ##label KO3
##cross-references GB:X57784
this sequence has been revise
$38721
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**cross-references EMBL:X57784; NID:g436061; PID:g436062

A48173
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Complete sequence of the desmoglein precursor and evidence for the existence of different desmoglein genes expressed in cell type-specific patterns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, February 1991 S38721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cowin, P. Biochem. Biochem. Res. Commun. (1990) 173:1224-1230
             #superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
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                                                                                                                                                                                                                                                    glycoprotein, as a member of the cadherin adhesion molecules.
                                                                                                                                                                                                                                                                                                                Zimbelmann, R.; Franke, W.W. 17. Cell Biol. (1990) 53:1-12
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transmembrane protein
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J. Cell Sci. (1991) 99:809-821
Structural analysis and expression
Structural component of the de
                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800 Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, is related to the cadherin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      desmoglein 1 precursor - human
desmosomal glycoprotein I
#formal_name Homo sapiens #common_name man
30-Jun-1993_#sequence_revision 30-Jun-1993
Wheeler, G.N.; Buxton, R.S.; Parker, A.E. Rees, D.A.; King, I.A.; Magee, A.I. Blochem. Soc. Trans. (1991) 19:1060-1064 Desmosomal glycoproteins I, II and III:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Wheeler, G.N.; Parker, A.E.; Thomas, C.L.; Ata Poynter, D.; Arnemann, J.; Rutman, A.J.; Pid Watt, F.M.; Rees, D.A.; Buxton, R.S.; Magee,
                                                                                                                                                                                                                              Nilles, L.A.; Parry, D.A.D.; Powers,
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#domain cadherin repeat homology #label CRI\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR4\
#domain cadherin repeat homology #label CR4\
#domain transmembrane #status predicted #label INT\
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                                                                                               26-1049 ##label NIL
                                                                                                                                                                                                                                                                                       24-1049 ##label WHE
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tdomain desmoglein repeat *label DG2\
tdomain desmoglein repeat *label DG3\
tdomain desmoglein repeat *label DG4\
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                                                                                                                                                                        of human desmoglein: a
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                                                       A.E.;
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#map_position 18q12.1-18q12.2
CLASSIFICATION #superfamily cadherin; cadherin
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Best Local
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                                    ##cross-references GB:S64273
                                              ##molecule_type mRNA
##molecule_type mRNA
777-1117 ##label KOC
                                                                                                                                                                                                                                                              ##molecule_type mRNA
1-1117 ##label ZIM
##cross-references EMBL:Z28317; NID:g416177; PID:g416178
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##residues 1-55 ##label WH3
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Similarity 80.0%;
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                                                                                                                                                                  Franke, W.W.

Eur. J. Cell Biol. (1991) 55:200

Complete amino acid sequence of
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calcium binding; cell adhesion; duplication; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Homo sapiens #common_name man
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997

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                                                                                                                                                                                                                           Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann,
                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, September 1993
                                                                                                                                                                                                                                                                                                                                                                                        Zimbelmann, R.
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                                                                                                     precursor polypeptide and identification of a second type of desmoglein gene.
ss MUID:92037656
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#domain propeptide #status predicted #label PRO\
#product desmoglein #status predicted #label MAT\
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domain cadherin repeat homology #label CR4\
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domain cadherin repeat homology *label CR2\
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desmoglein repeat *label DG2\
desmoglein repeat *label DG3\
desmoglein repeat *label DG3\
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Pred. No.
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Best Local S
Matches 1
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Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                               #journal
#title
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                                        *cross-references_MUID:87315445
*accession $04528
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                                                                                                                                                                                                                                                                                                                                                                                                            262 VDSKISYEIITQNPG 276
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p_position 18q12.1-18q12.2
##molecule_type mRNA
#residues 1-412,'V',414-884 ##label NAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
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similarity 73.3%;
11; Conservative
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T02501
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calcium binding; cell adhesion; duplication; glycoprotein;
                                                                          Transformation of cell adhesion introduced E-cadherin cDNA.
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#length 1117
                                                                                                                                                                      S04528; S03160; I49565; S48735
S04528
                                                                                                                                                                                                       #formal_name Mus musculus *common_name house mouse
30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change
13-Mar-1997
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                                                                                                               Nature (1987) 329:341-343
                                                                                                                                               Nagafuchi, A.; Shirayoshi, Y.; Okazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #length 1421 #molecular-weight 154325 #checksum
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#domain cadherin repeat homology #label CR2
yth 1117 #molecular-weight 122384 #checksum
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al protein T19C21.7 - Arabidopsis thaliana
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Pred. No. 8.47e-05;
3; Mismatches 1
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                                                                                             properties
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2 NSKIAFKIVSQEP 14

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##cross-references EMBL:X06115
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#cross-references MUID:92107977
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#cross-references_MUID:95010732
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#accession S03160
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##cross-references GB:M81449; NID:g192325; PID:g192326
299 NAAIAYTIVSQDP 311
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##cross-references EMBL:X06339
##note part of this sequence, including the amino
mature protein, was confirmed by protein
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##residues 156-300 ##label TON
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                                                                                          Local Similarity
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Lottspeich, F.; Engel, J.; Doelz, R.; Jaehnig, F.; Epplen,
J.; Mayer, S.; Mueller, C.; Kemler, R.
EMBO J. (1987) 6:3647-3653
The structure of cell adhesion molecule uvomorulin. Insights
into the molecular mechanism of Ca(2+)-dependent cell
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The E-cadherin promoter: Functional analysis of a G-C-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
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larity 61.5%;
Conservative
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#domain cadherin repeat homology #label CR1\
#region cadherin binding #status predicted\
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#domain cadherin repeat homology #label CR4\
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#domain propeptide #status predicted #label PRO\
#pproduct E-cadherin, epithelial #status experimental
#label MAT\
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Best Local Similarity 61.5%;
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##note the nucleotide sequence was
Library, August 1992
                                                                                                    ##cross-references EMBL:X54315
this sequence has been
                                                                                                                                                                                                                                                                    ##cross-references EMBL:X54315; NID:g34998; PID:g34999
NCE S11487
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##residues 1-906 ##label REI
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1-340,'N',342-698,'R',700-704,'F',706-906 ##label RE2
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Nucleic Acids Res. (19
Human N-cadherin: nuc
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N-cadherin; neuronal cadherin
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The structure of the gene coding for the mouse cell
                               D.; Spurr, N.; Goodfellow, P.
J. Neurochem. (1990) 55:805-812
                                                                    Walsh, F.S.; Barton, C.H.; Putt, W.;
                                                                                       JQ0751
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submitted to the EMBL Data Library, November
                                                                                                                                                                                                                                                                                                                                                                                                                A38870;
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#length 884 #molecular-weight 98283 #checksum
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                  N-cadherin gene maps to human
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to the E-cadherin gene.
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Pred. No. 4.53e-01
                                                                                                                                                                                                                nucleotide
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(1990) 18:5896
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##molecule_type mRNA
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##cross-references SGD:S0004489; MIPS:YML027w
#map_position 13L
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                                       #gene
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;72,622,651,692
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Similarity 46.7%;
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homeotic protein YOX1 - yeast (Saccharomyces cerevisiae)
protein YML027w
                                                                                                                                                                              Chromosoma (1993) 102:174-179
In vitro binding to the leucine
yeast homeobox gene.
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calcium binding; cell adhesion; duplication; glycoprotein;
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13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change
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                                                                             1-290,'QGLIIP' ##label KAU
es EMBL:X62392; NID:g5501;
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#domain cadherin repeat homology *label CR1\
*region cadherin binding *status predicted\
#domain cadherin repeat homology *label CR2\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR5\
#domain cadherin repeat homology *label CR5\
#domain transmembrane *status predicted *label INT\
#domain intracellular *status predicted *label INT\
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Pred. No. 4.53e-01
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#journal DNA Res. (1996) 3:109-136

Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

#cross-references_MUID:97061201
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##molecule_type
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PID:g1651744
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similarity 38.5%;
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                                                                                                       hypothetical protein G2842
#formal_name Saccharomyces cerevisiae
17-May-1996 #sequence_revision 17-May-1996
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                                                                                                                                                      s64146 #type complete probable membrane protein cerevisiae)
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                             submitted to the
                                                                         S64146; S71739
                                                                                                                                                                                                                                                                                                                                                                              #superfamily hypothetical protein s1r0725
#length 138 #molecular-weight 16580 #ch
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6803)
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#length 385
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ne Protein :
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Pred. No. 1.15e+00;
7; Mismatches 1
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                               Mazon, M.J.
ase, May 1996
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Best Local Similarity 42.9%;
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     36-4583
51-156
159-270
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##cross-references GB:M80537
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##cross-references EMBL:X92670
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##cross-references GB:M80537
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Cell (199)
                                                                                                                                              *superfamily cadherin-related tumor suppressor; cadherin repeat homology; EGF homology calcium binding; cell adhesion; duplication; transmembra
                                                                                                                                                                                                                                                                                                                                                                                                                                              The fat tumor suppressor gene in Drosophila encodes member of the cadherin gene superfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Drosophila melanogaster)
#formal_name Drosophila melanogaster
30-Sep-1993 #sequence_revision 30-Sep
16-Feb-1997
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#product cadherin-related tumor suppressor #status predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR2\
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Library, October 1995
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Pred. No. 1.81e+00;
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Best Local Similarity 50.0%;
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#title
#cross-references MUID:98065943
#accession F70126
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                       Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.;
Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.;
Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb,
J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.;
Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Vugt, R. V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman,
J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst,
K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.
Nature (1997) 390:580-586
Genomic sequence of a Lyme disease spirochaete, Borrelia
burgdorferi.
                                                                                                                                                                                                                                                                                          F70126 #type complete translation elongation factor P (efp) homolog - Lyme disease
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                                                                                                                                                                                                                                                               spirochete
#formal_name Borrelia burgdorferi #common_name Lyme disease
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##residues 1-877 ##label LIA
##residues 1-877 ##label LIA
##cross-references EMBL:X53615; NID:g164; PID:g664894
##Cadherins mediate calcium-dependent intercellular adhesion, and
thought to be involved in the sorting of different cell types
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Pred. No. 6.93e+00;
7; Mismatches 2
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*title Characterization and chromosomal localization of the gene

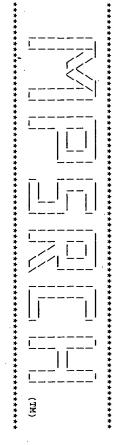
#cooding the human cell adhesion molecule uvomorulin.

#cross-references MUID:89031725
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#cross-references MUID:95324920
#accession A57171
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                                                                                                                          ##cross-references GB:L34784
                                                                                                                                                ##residues
                                                                                                                                                               ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type protein
##residues 'XQ',157-162,'V',164-179 ##label WHE
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##residues 157-311 ##label MAN
##cross-references EMBL:X12790
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##residues 265-392 ##label FRI
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Genomics (1995) 26:281-289
Cloning and characterization of the I
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submitted to the EMBL Data Library,
Sequence of human E-cadherin cDNA.
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ARC-1; cell CAM 120/80; E-cadherin; epithelial cadherin;
Rimm, D.L.; MORTOW, J.S.
Biochem. Biophys. Res. Commun. (1994) 200:1754-1761
MOlecular cloning of human E-cadherin suggests a nov
subdivision of the cadherin superfamily.
nces MUID:94242050
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Mol. Biol. Rep. (1993) 17:123-128
Molecular cloning and characterization of the human
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Soluble 80-kd fragment of cell-CAM 120/80 disrupts cell-cell
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                                                                                                                                                                                         sequence not shown; translation
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                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross references GDB:120484; OMIM:192090 #map_position 16q22.1-16q22.1 #introns 379/1.4467
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#cross-references MUID:94380041
#accession I52294
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297 NAAIAYTILSQDP 309
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##rresidues 1-16 ##label RES
##cross-references GB:L34545; NID:g509604; PID:g509605
NCE 152704
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T Cadherins mediate calcium-dependent intercellular adhesion and are
thought to be involved in the sorting of different cell types
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##residues 337-476 ##label RE2
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                                                                                              Match 56.3%;
Local Similarity 53.8%;
local 7; Conservative
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Cancer Res. (1994) 54:3845-3852
E-cadherin gene mutations provide clues to diffuse type
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                                                                                                                                                                                             predicted
#length 882 #molecular-weight 97455 #checksum 5112
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calcium binding; cell adhesion; duplication; glycoprotein;
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the majority of differences between this and other reports represent apparant frameshift errors
the authors translated the codon CCG for residue 868
                                                                                                                                                                                                                                               #binding_site carbohydrate (Asn)
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Search completed: Fri Jun 11 17:26:59 1999 Job time: 88 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:22:45 1999; MasPar time 2.44 Seconds 173.855 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-991-628-3 (1-15) from US08991628.pep 96 LNSKIAFKIVSQEPA 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 26.281; Variance 28.608; scale 0.919

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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51.0	51.0	51.0	51.0	51.0	51.0	51.0	51.0	51.0	51.0	52.1	52.1	52.1	52.1	52.1	52.1	52.1	53.1	53.1	53.1	54.2	54.2
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RETINAL-CADHERIN PRECU	RETINAL-CADHERIN PRECU	RETINAL-CADHERIN PRECU	NEURAL-CADHERIN 1 PREC	HYPOTHETICAL 67.5 KD P	BILIRUBIN OXIDASE PREC	APOCYTOCHROME F PRECUR	APOCYTOCHROME F PRECUR	ACYL TRANSFERASE (EC 2	RRNA ADENINE N-6-METHY	GENOME POLYPROTEIN 1 [GENOME POLYPROTEIN 1 [TRANSITIONAL ENDOPLASM	VACB PROTEIN.	PROBABLE METHYLTRANSFE	CARBONYL REDUCTASE [NA	ASPARTIC PROTEINASE IN	ISOCITRATE DEHYDROGENA	HYPOTHETICAL 74.5 KD P	SURFACE PRESENTATION O	CALPAIN P94, LARGE [CA	CALPAIN P94, LARGE [CA
1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.96e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01.	1.23e+01	7.62e+00	7.62e+00	7.62e+00	4.69e+00	4.69e+00
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EMBL; M76482; G190752; PIR; A41088; IJHUG3. MIM; 169615; PROSITE; PS00232; CADHERIN; 3. PFAM; PF00028; cadherin; 4. HSSP; P09803; 1EDH.	his SWISS-PROT entry is copyrige tween the Swiss Institute of the European Bioinformatics Institution se by non-profit institution oddified and this statement is nontities requires a license agreer send an email to license@isbreen.	-!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS (POTENTIAL). -! DISEASE: PENCHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.	SEQUENCE FROM N.A. MEDLINE; 92069753. MEDLINE; 92069753. *AMAGAI M., KLAUS-KOVTUN V., STANLEY J.R.; *AUTOANTIDODIES against a novel epithelial cadherin in pemphigus *PRINCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. -!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. -!- INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. -!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND CARCINAMAS	LT 1 DSG3_HUMAN STANDARD; PRT; 999 AA. P32926 01-OCT-1993 (REL. 27, CREATED) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DESMOGLEIN 3 PRECURSOR (130 KD PEMPHICUS VULGARIS ANTIGEN) (PVA). DSG3. ADTIENS (HUMAN). BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

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Q03763;
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REPEAT
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SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D., ZIMBELMANN R., FRANKE W.
KOCH P.J., MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
SEQUENCE OF 44-493 FROM N.A.

MEDILINE; 91097553.

GOODMIN L., HILL J.E., RAYNOR K., RASZI L., MANABE
GOODMIN L., HILL J.E., RAYNOR K., RASZI L., MANABE
"Desmoglein shows extensive homology to the cadheri
adhesion molecules.";
BIOCHEM. BIOPHYS. RES. COMMUN. 173:1224-1230(1990).
-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS
FILAMENTS MEDIATING CELL-CELL ADHESION.
                                                                                                                                                                                                  SEQUENCE OF 44-1043 FROM N.A. TISSUE-MUZZLE EPITHELIUM; MEDLINE; 91168965.
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                                                                                  polypeptide and EUR. J. CELL BIC
                                                                                                                                                           "Identification of desmoglein, a glycoprotein, as a member of the molecules.";
                                                                                                                                                                                                                                                                                     EUKARYOTA;
                                                                                          "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene.
                                                                                                          FRANKE W.W.;
                                                                                                                                   REVISIONS,
                                                                                                                                                                                             KOCH P.J.,
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                                                                                                                                                                                  IMBELMANN R., FRANKE W.W.;
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ARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
PECORA; BOVOLDEA; BOVOLDEA; BOVIDEA;
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                                                                                  identification of a second DL. 55:200-208(1991).
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                                         MANABE M. cadherin
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                  JUNCTIONS
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CONFLICT
SEQUENCE
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CARBOHYD
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DOMAIN
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PROPEP
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Q02413;
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EMBL; X58466; G307; -.
EMBL; X57784; G436062; -.
EMBL; M58165; G552318; -.
PIR; S14603; IJBGG1.
PROSITE; PS00232; CADHERIN; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are n use by non-profit institutions as long as its c modified and this statement is not removed. Usage entities requires a license agreement (See http://w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND
-i- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00028; cadherin;
HSSP; P09803; 1EDH.
CELL ADHESION; SIGNAL; T
CALCIUM-BINDING; REPEAT
                                                                                                                                                       01-OCT-1993 (REL. 27, C
01-OCT-1993 (REL. 27, L
01-NOV-1997 (REL. 35, L
DESMOGLEIN 1 PRECURSOR
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ARNEMANN J., RUTMAN A.J. BUXTON R.S., MAGEE A.I.;
                TISSUE-KERATINOCYTES;
MEDLINE; 91271279,
WHEELER G.N., PARKER A.E.,
ARNEMANN J., RUTMAN A.J.,
                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                           190 LNSKIAFKIIRQEPS
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SIMILARITY: BELONGS TO
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                                                                                                                                                                                                                                  STANDARD;
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27, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
URSOR (DESMOSOMAL GLYCOPROTEIN 1)
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Pred. No. 5:65e-09;
2; Mismatches 1
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CYTOPLASMIC
CADHERIN 1.
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WW; 13898584 CRC32;
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EXTRACELLULAR
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                   D.A.,
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MBL outstation -
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PROC. NATL.
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MIM; 125670; -.
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                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                           01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DESMOGLEIN 2 PRECURSOR (HDGC).
                                                                                                            DSG2_HUMAN
Q14126;
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REPEAT
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HSSP; P09803; 1EDH
CELL ADHESION; SIGN
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  EQUENCE
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FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.

INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE
FILAMENTS MEDIATING CELL-CELL ADHESION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND OESOPHAGUS.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE
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180
1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL;
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the cadherin family
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Pred. No. !
2; Mismai
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DESMOGLEIN REPEAT 2.
DESMOGLEIN REPEAT 4.
DESMOGLEIN REPEAT 5.
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                                                                                                                       PRT;
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5.65e-09;
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Matches 1
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUR. J. CELL BIOL. 55:200-208(1991).

-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUN INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND FILAMENTS MEDIATING CELL-CELL ADHESION.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY -I- TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND -I- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOCH P.J., GOLDSCHMIDT M.D., WALSH M.J., ZIMBELMANN R., FRANKE W.W.; "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene."; EUR. J. CELL BIOL. 55:200-208(1991).
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HSSP; P15116; 1NCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHAEFER S., KOCH P.J., FRANKE W.W.;
"Identification of the ubiquitous human desmoglein, Dsg2, and the expression catalogue of the desmoglein subfamily of desmosomal cadherins.";
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                               CYTOSKELETON;
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                      191 LNSKISYRIVSLEPA 205
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.
LNSKIAFKIVSQEPA
                                            n 80.2%;
Similarity 73.3%;
11; Conservative
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Pred. No. :
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DESMOGLEIN
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                                                                                          POTENTIAL.
W; 84D3B898 CRC32;
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EXTRACELLULAR
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                                             Mismatches
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AND INTERMEDIATE
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CARCINOMAS.
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RESULT 5
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STANDARD;

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01-MAR-1989 (REL. 10, 0
01-MAR-1989 (REL. 10, 1
15-JUL-1998 (REL. 36, 1
EPITHELIAL-CADHERIN PRI
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01-MAR-1989 (REL.
01-MAR-1989 (REL.
15-JUL-1998 (REL.
                                                                                                                                                                                                                                             OVERDUIN M., TONG K.I., KAY C.M., IKURA M.;

"1H, 15N and 13C resonance assignments and monomeric structure of the maino-terminal extracellular domain of epithelial cadherin.";

J. BIOMOL. NMR 7:173-189(1996).

-i- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92107977.
BEHRENS J., LOEWRICK O., KLEIN-HITPASS L., BIRCHMEIER W.;
"The E-cadherin promoter: functional analysis of a G.C-rich region and an epithelial cell-specific palindromic regulatory element.";
PROC. NATL. ACAD. SCI. U.S.A. 88:11495-11499(1991).
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"The structure of the gene coding for
molecule uvomorulin.";
NUCLEIC ACIDS RES. 19:6533-6539(1991).
                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 157-260
                                                                                                                                                                                                                                                                                                                                                                                                                                          dimerization."
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96176249.

NAGAR B., OVERDUIN M., IKURA M., RINI J.M.;
"Structural basis of calcium-induced E-cadherin rigidification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The structure of cell adhesion molecule uvomorulin. Ins the molecular mechanism of Ca2+-dependent cell adhesion. EMBO J. 6:3647-3653(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECTENCE OF 174-884 FROM N.A., AND SEQUENCE OF 157-181. MEDLINE; 88111553.
RINGWALD M., SCHUH R., VESTWEBER D., EISTETTER H., LOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-129/SV
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NATURE 329:341-343(1987).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
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                                                                                             the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                            SORTING OF HETEROGENEOUS CELL TYPES.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: NON-NEURAL EPITHELIAL TISSUES.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                           SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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G50765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R., VESTWEBER D.,
JAEHNIG F., EPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ), CREATED)
), LAST SEQUENCE UPDATE)
5, LAST ANNOTATION UPDATE)
PRECURSOR (E-CADHERIN) (UVOMORULIN) (ARC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R D., EISTETTER H., L.
EPPLEN J., MAYER S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF 157-370.
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                                                                        There are no restrictions ong as its content is in
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Matches
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Best Local
                                                                                                                                      CAD2_HUMAN STANDARD; PRT; 906 AA.

P19022; Q14923;
01-902-1990 (REL. 16, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NEURAL-CADHERIN PRECURSOR (N-CADHERIN).
CDH2 OR CDHN OR NCAD.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTPRAMATES; CATARRHINI; HOMINIDAE; HOMO.
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DOMAIN
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                         REID R.A., HEMPEKLA C.C., "Human N-cadherin: nucleotide and dequestion of the Nucleic ACIDS RES. 18:5896-5896(1990).
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TRANSMEM
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EMBL;
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PROSITE; PS00232; CADHERIN;
REVISIONS TO 341;
REID R.A.;
                                                                                           SEQUENCE FROM N.A. MEDLINE; 91016946.
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PFAM; PF01049; Cadherin_C_term;
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Similarity 61.5%;
8; Conservative
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Pred. No.
3; Misma
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SER-RICH.
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Mismatches 2;
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CRC32;
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EMBL; X57548; E31840; -.
EMBL; X54315; G34999; -.
EMBL; X2303; G253483; -.
EMBL; M34064; G416293; -.
EMBL; 227420; G806346; -.
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GENOMICS 22:172-179(1994)
-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
-1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
-1- FUNCTION: CADHERINS ARE THUS CONTRIBUTE TO THE MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED INSURANCE.

NEURONAL RECOGNITION MECHANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE;
                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
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WALLIS J.
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                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WALSH F'S., BARTON C.H.,
SPURR N., GOODFELLOW P.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no rest
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MEDLINE; 92363956.
SALOMON D., AYALON O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-20 FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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90347462.
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   FOX M., WALSH F.S.;
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   FROM N.A.
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CADHERIN 1.
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EXTRACELLULAR (POTENTIAL).
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N-cadherin
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P34161;
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                                                                                                           PFAM;
                                                                                                                                                    EMBL; X62392; G5502; -. EMBL; Z46659; G575692; -. PIR; S33388; S33388. SGD; L0002540; YOX1.
                                                                                                                                                                                                                                                                                                                             BADCOCK K., CHURCHER C., BARRELL B.G., RAJANDREAM M.A., WALSH SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: IN VITRO, IS CAPABLE OF BINDING TO THE DNA OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O1-FEB-1994 (REL. 28, CREATED)
O1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HOMEOBOX PROTEIN YOX1.
                                                                                                                              PROSITE; PS00027; PROSITE; PS50071;
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                             homeobox gene.";
CHROMOSOMA 102:174-179(1993).
                                                                                                                                                                                                                                                                                                                                                                                                               "In vitro binding to the leucine tRNA gene identifies a
                                                                                                                                                                                                                                                                                                                                                                                                                               KAUFMANN E.
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                                                                                              номеовох;
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364 KFGFKIVDQQP 374
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SUBCELLULAR LOCATION: NUCLEAR
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                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 92069752. MAHONEY P.A., WEBER GOODMAN C.S.;
                                                              "The fat tumor suppressor gene in Drosophila encodes a novel membe of the cadherin gene superfamily.";
CLLL 67:853-868(1991).
-i- FUNCTION: COULD FUNCTION AS A CELL-ADHESION PROTEIN.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- DISEASE: RECESSIVE LETHAL MUTATIONS IN FAT CAUSE HYPERPLASTIC,
TUMOR-LIKE OVERGROWTH OF LARVAL IMAGINAL DISCS, DEFECTS IN
DIFFERNTIATION AND MORPHOGENESIS, AND DEAT DURING THE PUPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P53125;
p53125;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1996 (REL. 37, LAST ANNOTATION UPDATE)
14POTHETICAL 145.6 KD PROTEIN IN RPL1B-CEG1 INTERGENIC REGION.
YGL133W OR G2842.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
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MEDLINE; 96437978.
ESCRIBANO V., ERASO P., PORTILLO F., MAZON M.J.;
"Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces cerevisiae chromosome VII reveals SEC27, SSM1b, a putative S-adenosylmethionine-dependent enzyme and six new open reading
                                                                                                                                                                                                                                       DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
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YEAST 12:887-892(1996).
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  DIFFERENTIATION AND MORPHOGENESIS, AND DEAT DURSTRACE.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
SIMILARITY: CONTAINS 37 CADHERINS-TYPE REPEATS.
SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
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larity 42.9%;
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33, LAST SEQUENCE UPDATE)
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PFAM; PF00028; cadherin; PFAM; PF00054; laminin_G; HSSP; P00740; lIXA.
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Y SIMILARITY.
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SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE; 98065943.
FRASER C.M., CASJENS S.,
                                                                                                                                                                                                                   1520 LNGKVSYAISKQEP 1533
                                                      BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)
BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; BORI
                                                                                                                                                                                               LNSKIAFKIVSQEP
                                                                                                                                                                                                                                          h 59.4%;
Similarity 50.0%;
7; Conservative
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7, LAST ANNOTATION
(EF-P).
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                                                                                                                           CREATED)
  HUANG
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Pred. No. 3.
4; Mismatc
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S -> G.
G -> S.
MW; 1EF20E
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                                                       BORRELIA
 G.G.,
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between
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DOUGHRATY B., TOMB J.F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKEMBUSH J., SALZBERG S.,
VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTTERBACK T., WAITHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH
SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAD2_BOVIN P19534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            burgdorferi.";
NATURE 390:580-586(1997).
                                                                                                                                                                                                                                                                 EMBO
                                                                                                                                                                                                                                                                                       MEDLINE; 90360979.
LIAW C.W., CANNON C., POWER "Identification and cloning endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDAT
NEURAL-CADHERIN PRECURSOR (N-CADHERIN) (FRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01275; EFP; FALSE_NEG.
PROTEIN BIOSYNTHESIS; ELONGATION FACTOR.
SEQUENCE 192 AA; 21413 MW; CB74964B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                    BOS TAURUS EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                ARTIODACTYLA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATE EFFICIENT TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED TOS RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERNING THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE (BY SIMILARITY).

PATHWAY: PROTEIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LNSKIAFKIVSQEPA
                                                                                                                   O J. 9:2701-2708(1990).
FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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Similarity 53.3%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                FROM N.A.
90360979.
                                                                                                                                                                                                                                                                                                                                                                                                 (BOVINE).
METAZOA; CHORDATA; VERTEBRATA; MA
METAZOA; CHORDATA; PECORA; BOVOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
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of two
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Pred. No. 1.04e+00;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                          KIBONEKA P.K., RUBIN L.L. o species of cadherins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UPDATE)
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A; BOVIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 192;
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; BOVINAE;
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PIR; S11693;
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SEQUENCE
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CARBOHYD
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or send a
MEDLINE: 89031725.

MANSOURI A., SPURR N., GOODFELLOW P.N., KEMLER "Characterization and chromosomal localization the human cell adhesion molecule uvomorulin."; DIFFERENTIATION 38:67-71(1988).

[4]
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                                                                                                                                          SEQUENCE OF 172-311
                                                                                                                                                                                  SUBMITTED
                                                                                                                                                                                                     SEQUENCE FROM N.A. KELKER W., WARDA A
                                                                                                                                                                                                                                                                                                                          SCHALKEN J.A.
                                                                                                                                                                                                                                                                                                                                           BUSSEMAKERS M.J.G.,
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 93211394.
                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 LNGMLRYRILSQAPS
                                                                                                                                                                                                                                                                                                     Molecular cloning
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                                                                                                                                                                                  (XXX-1992)
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                                                                                                                                                                                                                                                               REP. 17:123-128(1993)
                                                                                                                                                                                                       WARDA A.,
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larity 40.0%;
Conservative
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H5
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                                                                                                                                                                                                                                                                                                       characterization
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Pred. No. 1.74e+00;
7; Mismatches 2
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CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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SER RICH.
POTENTIAL.
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POTENTIAL.
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MEDLINE; 94306394.
BECKER K.-F., ATKINSON M.J., REICH
SIEWERT J.R., HOEFLER H.;
"E-cadherin gene mutations provide carcinomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94355985.

**RISINGER J.I., BERCHUCK A., KOHLER M.F., BOYD J.;

**MUTATIONS Of the E-cadherin gene in human gynecologic cancers.**,

NAT. GENET. 7:98-102(1994).

-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTI

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC

MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO

SORTING OF HETEROGENEOUS CELL TYPES. E-CADHERIN HAS A POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVIEW ON VARIANTS.

MEDLINE; 98415721.

BERX G., BECKER K.-F., HOEFLER H.,

"Mutations of the human E-cadherin
HUM. MUTAT. 12:226-237(1998).
                  PROPEP
CHAIN
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"Transcriptional regulation
prostate cancer cell lines:
gene promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-16 FROM N.A. MEDLINE; 94380041.
                                                                                                                                                                                                                                                                                    PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                             PIR; S25141; IJHUCE.
PIR; S37654; S37654.
MIM; 192090; -.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z13009; G31073; -.
EMBL; Z18923; G31075; -.
EMBL; X12790; G930046; -.
EMBL; L34545; G509605; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS THR-617; VAL-711 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOCHEM. BIOPHYS.
                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                       MIM; 192090;
PROSITE; PS00232; CADHERIN;
PROGOCOR: cadherin; 5.
                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVASIVE SUPPRESSOR ROLE.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: NON-NEURAL EPITHELIAL TISSUES.
DEFECTS OF CDH IS REGARDED AS ONE OF THE MAIN MOLECULAR
INVOLVED IN DYSFUNCTION OF THE CELL-CELL ADHESION SYSTEM,
TRIGGERING CANCER INVASION (GASTRIC, BREAST, OVARY, ENDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CADHERIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND
                                                                                                                                                                                                                                            ADHESION; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                PF00028; cadherin; 5.
PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THYROID) AND METASTASIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94380041.
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                                                                                                                                                                                                                                                               1SUH.
                                                                                                                                                                                                                       REPEAT;
  COMMUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L.A., VAN BOKHOVEN A., SCH
on of the human E-cadherin
s: characterization of the
                                                                                                                                                                                                                          SIGNAL;
                                                            CYTOPLASMIC CADHERIN 1. CADHERIN 2.
  CADHERIN
CADHERIN
CADHERIN
                                                                                                                                                                                                                                            PHOSPHORYLATION; TRANSMEMBRANE;
                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLY-838
                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                               E-CADHERIN
                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203:1284-1290(1994).
                                                                                                                                                                                                                          DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ч.
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                                            \omega \approx \mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BECKER I., NEKARDA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to diffuse type gastric
                                                                                                                                                                                                                          MUTATION
                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHALKEN J.A.;
rin gene in human
the human E-cadherin
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ENDOMETRIUM

EVENTS

cancers.";

PROTEINS

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Matches

REAL SECTION OF SECTIO

MOL.

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2SULT
D CADB_XENLA
C P33152;
C P33152;
OT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE BLASTOMERE-CADHERIN PRECURSOR (B-CADHERIN).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
THKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BAT
FUKARYOTA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
SERVICE COCCUS COCUS COCCUS COCUS COCCUS COC
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
CARBOHYD
CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                             MEDLINE; 9206281.

MEXPRESSION OF XBCAD, a novel cadherin, during oogenesis and early development of xenopus."

MECH. DEV. 35:33-42(1991).

MECH. DEV. 35:33-42(1991).

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES.

SORTING OF HETEROGENEOUS CELL TYPES.

SORTING OF HETEROGENEOUS CELL TYPES.

TISSUE SPECIFICITY: EXPRESSED IN PITUITARY GLAND, LUNG AND KIDNEY.

TISSUE SPECIFICITY: EXPRESSED IN PITUITARY GLAND, LUNG AND KIDNEY.

TO TISSUE SPECIFICITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
SEQUENCE
  EMBL; X78546; G468817; -. EMBL; X63719; G64567; -. PIR; S43065; S43065. TROSITE; PS00232; CADHERII
                                                                                                                                                                                                     the
                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MECH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MULLER H.A., KUHL M., FINNEMANN:
HAUSEN P., WEDLICH D.;
"Xenopus cadherins: the maternal
members of the family.";
                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 95151580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 459-905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 NAAIAYTILSODP
                                                                                                             send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Extended Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                        requires a license agreement (:
an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47:213-223(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                882 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309
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53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
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Pred.
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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. 1.74e+00;
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IN LOBULAR BREAST CANCER).

IN LOBULAR BREAST CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN THYROID CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).

IN DIFFUSE GASTRIC CANCER).
                                                                                                                           (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N ENDOMETRIAL CANCE
N OVARIAN CANCER).
N REF. 2).
CRC32;
                                                                                                                                                  Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BATRACHIA; ANURA;
                                                                                                                                                                                            restrictions
                                                                                                                                                  and
                                                                                                                                                                                                                      EMBL
                                                                                                                                                                                                                          a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                             .ch/announce/
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PRESULT RESULT REPORT OF THE COLOR OF THE CO
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIZINE; 89346748.

MIYATANI S., SHIMAMURA K., HATTA K., TAKE

"Neural cadherin: role in se
SCIENCE 245:631-635(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAD2_MOUSE
P15116;
01-APR-1990
01-APR-1990
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
                     "Structural basis of cell-cell adhesion by cadherins.";
NATURE 374:327-337(1995).
-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INVERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED I
NEURONAL RECOGNITION MECHANISM.
-!- SUBCELLULAR_LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR_LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                   MEDLINE; 95191680.
SHAPIRO L., FANNON A.M.,
GRUEBEL G., LEGRAND J.-F
HENDRICKSON W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM;
PFAM;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NEURAL-CADHERIN PRECURSOR (N-CADHERIN).
                                                                                                                                                                                                                                                                                                                      SUBMITTED (NOV-1997)
                                                                                                                                                                                                                                                                                                                                           TAMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RODENTIA; SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF MEDLINE; 95191680.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. 
TAMURA K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADHESION; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00028; cadherin; 5.
PF01049; Cadherin_C_term;
P09803; 1SUH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 56.3%;
Similarity 50.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 905
                                                                                                                                                                                                                          LEGRAND J.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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 entry
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905
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                                                                                                                                                                                                                                                                                                                        EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MURIDAE;
                                                                                                                                                                                                                          KWONG P.D., TH
                                                                                                                                                                                                                                                                                                                                                                                                                ., HATTA M.,
TAKEICHI M.;
n selective c
copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILT -> NSA (IN REF. R -> Q (IN REF. 2). V -> A (IN REF. 2). D -> N (IN REF. 2). D -> N (IN REF. 2). D -> N (IN REF. 2). MISSING (IN REF. 2).
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Pred.
4; M
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CYTOPLASMIC ()
SER-RICH.
ASP/GLU-RICH
POTENTIAL.
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POTENTIAL.
ILT -> NSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; MAMMALIA; EUTHERIA;
AE; MURINAE; MUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B-CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     re 54; DB 1; Le
d. No. 1.74e+00;
Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                   cell-cell adhesion.";
                                                                                                                                                                                                                            THOMPSON A.,
EN J., COLMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAGAFUCHI A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     906
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CRC32;
                                                                                                                                                                                                                                                                                   160-267
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C STRAIN-5288C / SEY6210;

X MEDLINE; 97060018.

A PAGE N., SHERATON J., BROWN J.L., STEWART R.S., BUSSI T "Identification of ASK10 as a multicopy activator of transcription of a HIS3 reporter gene.";

YEAST 12:267-272(1996).
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EMBL; AB008811; 1
PIR; A32759; IJM
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O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
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EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL ADHESION; GLYCOPROTEIN; PHOSPHORYLATION; TRANSMEMBRANE, CALCIUM-BINDING; REPEAT; SIGNAL; 3D-STRUCTURE.
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ASK10 OR YGR097W.
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CADHERIN 3.
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

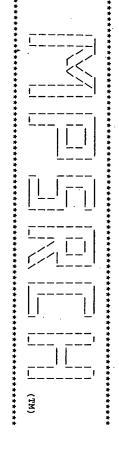
HERNANDEZ K., WEBER N., WIPFLI P., SCHMIDHEINI T.;

SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS

-I- FUNCTION: PUTATIVE ACTIVATOR OF SKN7.

-I- SIMILARITY: TO YEAST YILLOSC AND YNLO47C.
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Search completed: Fri Jun 11 17:22:53 1999 Job time : 8 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:23:10 1999; MasPar time 6.15 Seconds 133.169 Million cell updates/sec

Tabular output not generated.

Scoring table: Sequence: Description: Perfect Score: Title: >US-08-991-628-3 (1-15) from US08991628.pep 96 LNSKIAFKIVSQEPA 15

PAM 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 25.449; Variance 30.607; scale 0.831

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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T19C21.7 PROTEIN. T19C21.7 ROTEIN. T19C21.7 RAGIEOPHIANIAN (MOUSE-EAR CRESS). EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;	01-NOV-1	RESULT 2 ID 080907 PRELIMINARY; PRT; 1421 AA. AC 089907:	190 MNSKIAFKIVSQEPA 204 : 1 LNSKIAFKIVSQEPA 15	Query Match 95.8%; Score 92; DB 11; Length 993; Best Local Similarity 93.3%; Pred. No. 3.46e-09; Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	NON_TER 993 993 SEQUENCE 993 AA; 107888 MW; 881794BD CRC32;	PROSITE; PS00232; CADHEI PFAM; PF00028; cadherin; CELL ADHESION; GLYCOPRO?	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY). EMBL; U86016; G2290200;	STRAIN-BALB/C;			RESULT 1 ID 035902 PRELIMINARY; PRT; 993 AA. AC 035902;

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P72670

P72670;

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01-FEB-1997 (TREMBLREL 02, LAST SEQUE
01-NOV-1998 (TREMBLREL 08, LAST ANNOT
HYPOTHETICAL 16.6 KD PROTEIN.
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
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Q1-NOV-1996 (TREMBLREL. (
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E38B7.4 PROTEIN.
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STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L.,
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., A
SOMERVILLE C.R., VENTER J.C.;
"ALTABIdOpsis thaliana chromosome II BAC T19C21 ger
"SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BAN
EMBL; ACO04683; G3395428; -.
SEQUENCE 1421 AA; 154325 MW; 1B6D2FFI CRC32;
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EMBL; D90899; D1017405; -.
HYPOTHETICAL PROTEIN.
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[1]
                                                                CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
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RHABDITINA; [1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKIAFKIVSQEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYANOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JUN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRASSICACEAE; ARABIDOPSIS.
                                   RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
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02, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHROOCOCCALES;
                                DDA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIDA; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
8; M
                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 2; I
Pred. No. 7.46e-01;
7; Mismatches 1
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA436352 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     re 61; DB 10; I
d. No. 1.65e-01;
Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic sequence.";
BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADAMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                  A CONTRACTOR OF THE CONTRACTOR
                                                                                                                                                                                                                    SEQUENCE FROM N.A.

XX MEDLINE; 94150718 A.

XX MEDLINE; 94150718 A., ANDERSON K., BAYNES C., BERKS M.,

XX MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

XX MEDLINE; 94150714 A., CONNELL M., COPER J., COULSON A.,

XX CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

XX CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

XX GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

XX JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

XX LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XX LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XX LIGHTNING J., FLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XX ALLON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

XX SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON R.,

XX MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

XX WILSON BERKS M.,

XX WILSON BERKS M.,

XX MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

YALLON B., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

YALLON B., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Query Match
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Q93345;
Q93345;
Q1-FEB-1997
Q1-JAN-1998
Q1-JAN-1999
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C36B1.11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERT J., COOPER J., COULSO,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORFIMORE B., O'CALLAGHAN M.
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKE
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUGIN, CROPK THE MATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATURE 368:32-38(1994).
EMBL; Z74033; E1346602; -.
SEQUENCE 225 AA; 26356 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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MEDLINE; 94150718.
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                                                                                                               NATURE 368:32-38(1994).
EMBL; Z80215; E1344392; -
SEQUENCE 327 AA; 37139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENNARD N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 LASKVSFVRVSQVPS
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8; Conservative
     Similarity
8; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
  57.3%;
larity 80.0%;
Conservative
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53.38;
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                                                                                                                     ₹.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
     Pred.
1;
                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                  D8A2C259 CRC32;
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     Mismatches
                             No.
                                ; DB 5; I
. 3.21e+00;
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     Gaps
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RESULT 6

ID 048607;
AC 048607;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANOMATION UPDATE)
DE HYPOTHETICAL 12.3 KD PROTEIN (FRAGMENT).

OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TI
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; LILIOPSII
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; LILIOPSII
OC EUKARYOTA; VIRIDIPLANTAE; MAGNOLIOPHYTA; LILIOPSII
OC EUKARYOTA; HORDEUM.
RN [1]
RP SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ222776; E1203984; -.

KW HYPOTHETICAL PROTEIN.
FT NON_TER

1 1
SEQUENCE 108 AA; 12250 MW; E5FD23CE CRC32;
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     RESULT
AC Q
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DT Q
OC GEN Q
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                                                                     ULT 8
Q15855 PRELIMINARY;
Q15855; Q16194; Q13799;
01-NOV-1996 (TREMBLEEL. 01
01-NOV-1996 (TREMBLEEL. 01
01-NOV-1998 (TREMBLEEL. 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O55075 PRELIMINARY;
O55075; PRELIMINARY;
O55075; O1-JUN-1998 (TREMBLREL 06, C
O1-JUN-1998 (TREMBLREL 07, L
O1-AUG-1998 (TREMBLREL 07, L
N-CADHERIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRICETULUS GRISEUS (CHINESE HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
SCIUROGNATHI; MURIDAE; CRICETINAE; CRICETULUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                    LNSKIAFKIVSQEPA
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similarity 40.0%;
6; Conservative
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238 AA;
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larity 45.5%;
Conservative
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                                                                           01, CREATED)
01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
-CADHERIN) (ARC-1/UVOMORULIN).
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Pred. No. 5.
7; Mismatc
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Pred. No.
5; Misma
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        VERTEBRATA;
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1. No. 5.16e+00;
Mismatches 2;
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ANNOTATION UPDATE)
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5.16e+00;
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     MAMMALIA;
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LILIOPSIDA; POALES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
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        EUTHERIA;
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          PRIMATES;
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Best Local
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                                                                                                                                     guinea pigs.";
J. VET. MED. SCI
EMBL; AB012132;
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01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIMM D.L., MORROW J.S.;
"Molecular cloning of human
of the cadherin superfamily.
BIOCHEM. BIOPHYS. RES. COMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00232; CADHERIN; 3.

PRAM; PF00028; cadherin; 5.

PFAM; PF01049; cadherin_C_term; 1.

CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE;

CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE;

CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 94306394.
BECKER K.F., ATKINSON M.J.,
SIEWERT J.R., HOFLER H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 333-472 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATARRHINI;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (MAR-1990) TO EMBL/GENBANK/DDBJ-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRIXEN U.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94242050.
                                                                                                                                                                                                                                                             STRAIN-GP;
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                                                                                                                        SEQUENCE
                                                                                                                                                                                                  OHSAWA K., YAMADA A., TAKEUCHI K., WATANABE Y., MIYATA H., "Genetic characterization of parainfluenza virus 3 derived
                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   LARGE PROTEIN.
HUMAN PARAINFLUENZA VIRUS 3.
VIRUSES; SSRNA NEGATIVE-STRAND VI
PARAMYXOVIRIDAE; PARAMYXOVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF
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      866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 NAAIAYTILSQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L; S72397; E136801; JOINED.
L; L108599; G340188; -
L; S72492; E136801; -
L; S72491; E136801; JOINED.
L; X52279; G28822; -
LDRSVLYRIMNOEPG 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSKIAFKIVSQEP
                                                             Similarity
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3 (TREMBLREL.
9 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          878 AA;
                                                                                                                    132; D1033539;
2258 AA; 2588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261-388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                             SCI. 60:919-922(1998).
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                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        878 C
96741 MW;
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                                                           56.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                  8,88
                                      Score 54;
Pred. No.
7; Misma
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                                                                                                                        WW.
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LAST SEQUENCE UP
LAST ANNOTATION
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Pred.
4; M
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; 8F7F0180 CRC32;
                                                                                                                                                                                                                                                                                                                         VIRUSES; MONONEGAVIRALES; 
AE; PARAMYXOVIRUS.
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                                             Mismatches
                                                                                                                        8E00950F CRC32
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No. 5.16e+00;
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                                    DB 14; Len
.5.16e+00;
-tahes 3;
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O43159;
O1-JUN-1998 (TREMBLREL. (
O1-JUN-1998 (TREMBLREL. (
O1-AUG-1998 (TREMBLREL. (
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DURBIN A.D.;

SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ

EMBL; U51116; G1262234; -.

PFAM; PF00946; Paramyx_RNA_Pol; 1.

SEQUENCE 2258 AA; 258927 MW; 4B7A664B
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081081;
01-NOV-1996
01-NOV-1996
01-NOV-1998
                                                                                                                                                                                 ISHIKAWA K., NAGASE T., NAKAJIMA D., SEKI N., TANAKA A., KOTANI H., NOMURA N., OHARA O.; SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; AB007869; D1024586; -.

SEQUENCE 464 AA; 51479 MW; 4C0DDBCE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIAA0409,
HOMO SADIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIAA0409 (FRAGMENT).
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STOKES A., TIERNEY E.L., SARRIS C.M., MURPHY B.R., HALL The complete nucleotide sequence of two cold-adapted, temperature-sensitive attenuated mutant vaccine viruses cp45) derived from the JS strain of human parainfluenza
                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-JS;
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VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES; PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
      416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED
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                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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TKLGFKIVSKD
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                                                               Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MAR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30:43-52(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TREMBLREL. (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.3%;
33.3%;
                                                                                     55.2%;
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108,
101,
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                                                         Score 53; D
Pred. No. 8.
4; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; D
Pred. No. 5.
7; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA;
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4B7A664B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464
                                                                                     DB 4; I
8.24e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                       DATA BANKS
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                                                                                                                  Length 464;
                                                                                                                                                                                                                                                                                                                             OHIRA M.,
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                                                         Indels
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                                                                                                                                                                                                                                                                                                                                MIYAJIMA
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RESULT
AC QA
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                                                                                                          Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.2%;
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                             "Determination of the complete nucleotide sequence of the Sendal Virus genome RNA and the predicted amino acid sequences of the F, and L proteins.";

NUCLEIC ACIDS RES. 14:1545-1662/1007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL, 01, CREATED)
01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE
01-NOV-1998 (TREMBLREL, 08, LAST AUNOTATION UPDA
SENDAI VIRUS (STRAIN Z) GENOME RNA 5'END (STRAIN
HUMAN PARAINFLUENZA 1 VIRUS.
VIRUSES; SCRNA NEGATIVE-STRAND VIRUSES; MONONEGA
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
                                                                                                                                                                                                                                           NUCLEIC ACIDS RES. 14:1545-1563(
EMBL; X03614; G60900; -
PFAM; PF00946; Paramyx_RNA_pol;
SEQUENCE 1980 AA; 224006 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 13
Q84185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The gene family of subtilisin-like proteases in tomato."; SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; X98930; E259406; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AJ006379; E1299612; --
FFAM; PF00082; subtilase; 3.
MENDEL; 8813; LYCes;1086; 2.
PROTEASE; SERINE PROTEASE.
SEQUENCE 775 AA; 83115 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. VFW8;
MEICHTRY J., AMRHEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYCOPERSICON ESCULENTUM (TOMATO).

EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOP EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERINE PROTEASE,
                              725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         734 LSYKVTFKTVSROKA
                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LNSKIAFKIVSQEPA
LDKQVLYRVMNQEPG
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                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                        55.2%;
26.7%;
                              739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01, CREATED)
01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
GENOME RNA 5'END (STRAIN Z).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9,03,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WW;
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Pred.
                                                                                                  Score 53; DB 14; LA
Pred. No. 8.24e+00;
8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                            1
4BAC22B0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2EBF3C5E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1980
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8.24e+00;
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                                                                                                                                                                              Length 1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                      Indels
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                                                                                                      0
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RESULT 14

ID 055528

OC 05528

OT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE RNA POLYMERASE PROTEIN.

GN L.

OS SENDAI VIRUS.
OC VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES
OC VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES
OC PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.

RN [1]

RY SEQUENCE FROM N.A.
RC STRAIN-OHITA;
RX MEDLINE; 98062143.
RX MEDLINE; 98062143.
RT TIO1#*IO1 of an avirulent mutant of Sendai virus with
mutations from a highly virulent field strain through a

RT LLC-MK2 Cells.";
RL J. GEN. VIROL. 78:3207-3215(1997).
DR EMBL; AB005795; Dl025305; -.

SO SEQUENCE 2228 AA; 253058 MW; 8816E77F CRC32;
                                                                                                                                                                                                                                                                                                            RESULT 15

RESULT 15

AC 055530;

DT 01-JUN-1

DT 01-JUN-1

DT 01-NOV-1

DE RNA POLI

GN L.

OS SENDAI 1

OC VIRUSES;

CC PARAMYX

PARAMYX

PARAMYX

TON (1)

RC STRAIN-1

RT SEQUENCI

RC STRAIN-1

RT MITALIOH M.

RT ITOH M
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Best Local Similarity 26.7%;
Matches 4; Conservative
                                                                                                                                                      Query Match 55.2%;
Best Local Similarity 26.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98062143.

ITOH M., ISEGAWA Y., HOTTA H., HOMMA M.;

"ITOH M., ISEGAWA Y., HOTTA H., HOMMA M.;

"Isolation of an avirulent mutant of Sendal virus with two amino acid mutations from a highly virulent field strain through adaptation to LLC-MK2 cells.";

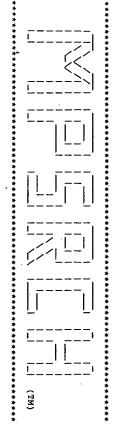
J. GEN. VIROL. 78: 3207-3215(1997).

EMBL; AB005795; D1025305; -.

EMBL; AB005795; D1025305 MW; 8816E77F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SENDAI VIRUS.
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
                                                                                                                                                                                                                                                                                                                ITOH M., ISBGAWA Y., HOTTA H., HOMMA M.;
"Isolation of an avirulent mutant of Sendal virus with two amino acid mutations from a highly virulent field strain through adaptation to LLC-MK2 cells.";
1. GEN. VIROL. 78:3207-3215(1997).

EMBL; ABOS796; D1025314;
-.
SEQUENCE 2228 AA; 253000 MW; A3058CCB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
RNA POLYMERASE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SENDAI VIRUS.
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE; 98062143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               973 LDKQVLYRVMNQEPG 987
                                                                             973 LDKQVLYRVMNQEPG 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LNSKIAFKIVSQEPA 15
        μ
LNSKIAFKIVSQEPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                        253000 MW; A3058CCB CRC32;
                                                                                                                                                          Score 53; DB 14; Length 2228; Pred. No. 8.24e+00; 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 14;
Pred. No. 8.24e+00;
8; Mismatches 3
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Search completed: Fri Jun 11 17:25:14 1999 Job time : 124 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm MasPar time 4.88 Seconds 65.408 Million cell updates/sec

Fri Jun 11 17:34:04 1999;

Tabular output not generated. Run on:

Description: Perfect Score: Title: 108 >US-08-991-628-4 (1-15) from US08991628.pep

Scoring table: PAM 150 Gap 15 Sequence:

1 TPMFLLSRNTGEVRT 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseg35

34:part34 39:part39 i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part14 15:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 23:part25 26:part26 27:part27 23:part28 29:part29 30:part20 31:part31 32:part37 38:part38 34:part34 35:part35 36:part36 37:part37 38:part38

Statistics: Mean 19.257; Variance 58.572; scale 0.329

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

W

Result No.	Score	Query Match	Length	₽B	ID	Description	Pred. No.
ב	108	100.0	15	မ္	W78815	Desmoglein 3 protein	6.54e-05
2	108	100.0	15	20	W04844		6.54e-05
ω	108	100.0	15	ü	W64816		6.54e-05
4	108	100.0	614	19	W07908	Pemphigus vulgaris an	6.54e-05
ر ن	108	100.0	999	σ	R30742	Human pemphigus vulga	6.54e-05
O	88	81.5	778	21	W15489	Pemphigus foliaceus a	1.64e-02
7	61	56.5	583	Ŋ	R07999	Asparagine synthetase	1.82e+01
89	61	56.5	586	N	R07998	Asparagine synthetase	1.82e+01
9	60	55.6	163	34	W38654	S. pneumoniae asparta	2.33e+01
10	59	54.6	616	17	R86867	Rat protocadherin pc5	2.98e+01
11	57	52.8	. 263	24	W13010	Segment of desmosomal	4.84e+01
12	57	52.8	560	24	W13009	Segment of desmosomal	4.84e+01
13	55	50.9	660	13	R69633	Human interleukin-12	7.81e+01
14	55	50.9	662	13	R69632	Human interleukin-12	7.81e+01
15	55	50.9	662	21	W12772	Human interleukin-12	·7.81e+01
16	54	50.0	325	28	W33725	Mouse melanocortin-5	9.91e+01

44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	. 18	17
50	50	50	50	50	50	50	50	50	50	50	51	51	51	51	5 ω	54	54	54	54	54	54		54	54	54	54	54
46.3	46.3	46.3	46.3	46.3	46.3	46.3	46.3	46.3	46.3	46.3	47.2	47.2	47.2	47.2	49.1	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
878 15 928 22	0					405																					
5 R85487 2 W21017				R7992		P3020	קי						R2401		P3020	W8513	W8415	W8415	W8513				W7968		R7950		
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Human E-c H. pylori	Lactobacillus	Human retinoid	Farnesoid-activated	Porcine a	Sequence encoded	Sequence encoded	Fusion protein contg	Sequence of	Hook region	Sequence of	Phosphatidyl	Human class	Fusion pr	Humam GM-CSF	Sequence encoded	A desaturase enzyme		Human des	A desaturase	Human desaturase		Human cyc	Melanocortin-5	lanocor	Rat melan	Mouse mel	Mouse mel
		inoid r	i-activa	acylglucosami	encoded	encoded	otein c		#	'n		SS II P	₩.	CSF rec	encoded	ase enz	desaturase	~		aturase	ase enzyme	-			melanocortin	melanocortin	melanocortin
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ALIGNMENTS

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C Pharmaceutical preparations for tolerisation to antigens comprise either an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to an autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II sequence corresponding to a sequence motif for a MHC class II protein, such as HIA-DR, which is associated with a human autoimmune disease and which binds to the polypeptide to activate autoreactive T-cells in individuals with the autoimmune disease. This peptide is charited from the human desmoglein a protein (amino acids 206-220) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein protein are described in W04841-47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                        29-SEP-1998 (first entry)
Desmoglein-3 206-220.
Desmoglein; DG; gene therapy; pemphigus vulgaris; autoantigen; autoimmune disease; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W04844 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into phagocytic cells. The treating genetic diseases, an immune response.
                              Homo sapiens.
US5783567-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 96-425218/42.
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07-MAR-1996; U03182.
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W09627387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;
pemphigus vulgaris; desmoglein; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Self epitope of desmoglein 3, implicated in autoimmune disease. Tolerisation; self-epitope; antigen; autoimmune disease;
                                                                                                                                       W64816 standard; peptide;
W64816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               auto-immune disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        herpes simplex virus; adenovirus; phosphomannomutase;
human papillomavirus; Epstein-Barr virus; DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE
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787547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wucherpfennig KW,
                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 108; DB 35;
Pred. No. 6.54e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                           Score 108; DB 20;
Pred. No. 6.54e-05;
0; Mismatches (
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                                                                                                                                                                                                                                         pemphigus
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids to phagocytic cells. In one embodiment the microparticles are less than 20 microns in diameter and the nucleic acid (preferably in closed circular form) includes an expression control sequence operatively linked to a coding sequence, where the expression product of the coding sequence is a polypeptide having a length and a sequence which permits it to bind to an MHC class I or II molecule. The expression product is thus an effective stimulator of an immune response in mammals. The present sequence, an antigenic portion of desmoglein 3, is an example of an MHC class II peptide which can be expressed by the nucleic acid. It is associated with pemphigus
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Disclosure; Column 4; 42pp; English.
The patent describes a new preparation of microparticles each
Comprising a polymeric matrix and a nucleic acid. The polymeric
matrix consists of one or more synthetic polymers having a solubility
in water of less than 1 mg/1 (e.g. poly-lactic-co-glycolic acid);
and at least 90% of the microparticles have a diameter of less than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PANG-) PANGAEA PHARM Curley JM, Hedley ML, WPI; 98-427077/36.
                                                                                                                                                                                                                                                                                           Fused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fattal if untreated. The PV antigen was fused to a human IgG1 hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pemphigus vulgaris antigen protein extracellular region. Autoantibody; immunoglobulin G; IgGl; fusion protein; ditreatment; pemphigus vulgaris; PV; bulla; blister; skin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-1997;
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                                                           205
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614 AA;
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larity 100.0%;
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No. 6.54e-05;
                                                                                                                                                  108; DB 19;
No. 6.54e-05;
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1057798918-A.
US7798918-A.
15-DEC-1992: 798918.
27-NOV-1991: US-798918.
PR 27-NOV-1991: US-798918.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
"" (USSH) US DEPT HEALTH & HUMAN SERVICE.
"" (USSH) US DEPT HEALTH & HUMAN SERVICE.
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                                                                                                                        remphigus foliaceus antigen-IgG constant region fusion protein - linked through the hinge region used to treat pemphigus foliaceus Claim I; Page 10-12; Typ; Japanese.

This sequence represents a fused protein recognised by pemphigus foliaceus this sequence represents a fused protein recognised by pemphigus foliaceus is a chronic perotein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion useful for detecting pemphigus foliaceus antibodies which is useful in immunocodiagnosis. The fusion protein has little or no side effects.
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Best Local S
Matches 1
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12-SEP-1995;
12-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1997 (first entry)
Pemphigus foliaceus antigen-IgG constant region fusion protein.
Pemphigus foliaceus; autoantibody; constant region; IgG;
extracellular region; antigen; hinge portion; skin;
dermatitis herpetiformis; fusion protein; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W15489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pemphigus vulgaris. It is thought that the adhesion molecule. Sequence 999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding pemphigus vulgaris a diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.
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Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-1993
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quence 778 AA;
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larity 100.0%;
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Pred. No. 6.54e-05;
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DB 21; Le..
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15-NOV-1990; U02443.
02-MAY-1999; U5-347302.
26-APR-1999; U5-514816.
(UYRO-) ROCKFELLER UNIV.
COTUZZI GM, TSAI FY;
WPI; 90-361471/48.
                                                                                                                                       R07998;
26-FEB-1991 (first entry)
Asparagine synthetase AS1.
asparagine synthetase; transgenic plant; herbicide resistance;
asparagine introgen fixation; pea.
                                                                                                                                                                                                                                                                                                                                     A comparison of pea AS and human AS polypeptides reveals homology of 47% at the amino acid level, c.f. 86% between AS2. There are several regions of high local homology (g. 80%) shared between the pea AS and human AS polypeptides see also Q06598, Q06622 and Q06623.
                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plants
Disclosure; Fig 2B; 91pp; English.
Disclosure; Fig 2B; 91pp; English.
The DNA sequence encoding this protein was isolated from cDNA
Clones selected from a pea nodule cDNA library from the "Sparkle"
variety of P.sativum. Pea ASI cDNA was used as a probe.
The protein is produced by expression vectors containing the AS2
coding sequence. Recombinant AS can be used to engineer herbicide
resistance, as a dominant selectable marker, to select novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asparagine synthetase AS2. asparagine synthetase; transgenic plant; drought tolerance; nitrogen fixation; per
                                                                                                                               Key
                                                                                                                                                                                            R07998 standard;
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26-FEB-1991 (first entry)
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Similarity 77.8%;
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in human
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% between AS1 and
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TRESULT OF THE STATE OF THE STA
PS Claim 12; Page 407; 483pp; English.

CThis sequence represents a Streptococcus pneumoniae protein that, based on homology with an Escherichia coli protein, is a aspartate ammonia con induction and is encoded by a DNA sequence of the invention.

CT ligase, and is encoded by a DNA sequence of the invention set rain of the invention can be used to identify compounds which interact with and continuous pneumoniae strain of the continuous pneumoniae proteins. Antagonists can be used to identify compounds which interact with and continuous pneumoniae proteins. Antagonists can be continuous to a tireat diseases caused by S. pneumoniae proteins, through genetic continuous pneumoniae proteins or delivery confirmed an ammonia by inoculation with the S. pneumoniae proteins or delivery confirmed immune responses to protect the animal from disease. The continuous can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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03-MAY-1989; US-347302.
26-APR-1990; US-514816.
(UYRO-) ROCKFELLER UNIV.
COTUZZÍ GM, TSAÍ FY;
WPI; 90-361471//o
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15-NOV-1990.
02-MAY-1990;
03-MAY-1989;
26-APR-1990;
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Disclosure; Fig 2A; 9lpp; English.
The DNA sequence encoding this protein was isolated from cDNA clones selected from a pea nodule cDNA library from the "Sparkle" variety of p. sativum. Human AS cDNA was used as a probe.
The protein is produced by expression vectors containing the AS1 coding sequence. Recombinant AS can be used to engineer herbicide resistance, as a dominant selectable marker, to select novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound;
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W38654;
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See also Q06599,
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14-MAY-1997; U07950.
14-MAY-1996; US-017670.
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Similarity 77.8%;
7; Conservative
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/label= putative glutamine binding
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EECHAM PLC.
, Knowles DJC,
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Pred. No. 1.82e+01
2; Mismatches
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                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                 Prolynucleotide(s) encoding human protocadherins pc3 and pc4 and rat profit involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell adhesion and regulation activities pc5 - fivelyed in cell-cell adhesion and regulation activities pc5 - fivelyed in cell-cell adhesion in three protocadherins. This cc R8885-R86867 represent the sequences for three protocadherins. This created to cadherin, and possess cell adhesive ability. Cadherins are crelated to cadherin, and possess cell adhesive ability. Cadherins are composed of an N-terminal extracellular domain cathering in the cell-cell adhesion. Cadherins are composed of an N-terminal extracellular domain continuous continuous composed of an N-terminal extracellular domain continuous continu
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Best Local Similarity
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R86867;
R86867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques. Sequence 163 AA;
                                      Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface;
carcinoma; desmogne; antibody; epitope; diagnosis; de
micrometastasis; separation; enrichment; targetted del
                                                                                                                                                                         W13010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suzuki S;
WPI; 96-068873/07.
N-PSDB; T03574.
                    micrometastasis; metastatic.
                                                                                                                                                         W13010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus rattus. WO9600289-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catenin; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1995; U08071.
27-JUN-1994; US-268161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat protocadherin pc5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DOHE~) DOHENY EYE INST.
Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1996
                                                                                                                                21-NOV-1997 (first entry)
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                                                                                                                                                                                                                                                                1 TPMFLLSRNTGEV
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                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                         protein;
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                                                                                                                                                                                                                                                                                                                                                                        54.6%;
                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                 Score 59; DB 17;
Pred. No. 2.98e+01;
3; Mismatches 2
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Pred.
3; M
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, 2.33e+01;
-hes 2;
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                                                                                                                                                                                                                                                                                                                                                                                            Length 616
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CC The present sequence is a segment of the desmosomal cadherin (DC), CC desmoglein Dsg2, which is exposed on the surface of epithelial or CC arcinoma cells and not bound to desmosomes. An antibody (Ab) CC directed against epitopes of the present sequence can be used to CC diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes. An ontibody of the present sequence can be used to CC diagnose, i.e. to detect carcinoma cells, especially concretastases, not bound to desmosomes, to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods and CC as a therapeutic to deliver agents, e.g. other Ab or toxins, to CC metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                         Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, we seem to fereigness and treatment of carcinoma micrometastases of claim 7; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC), and the desmosome of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) of carcinoma cells and not bound to desmosomes. An antibody (Ab) of carcinoma cells and not bound to desmosomes, an antibody (Ab) of carcinoma cells and not bound to desmosomes, to separate, enrich or detect living or fixed carcinoma cells, especially micrometastases, not bound to desmosomes, to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods and cas a therapeutic to deliver agents, e.g. other Ab or toxins, to metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
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Best Local
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(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaefer S;
WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaefer S;
WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithe carcinoma; desmosome; antibody; epitope; diagnosis; detectio micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
DE19531033-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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23-AUG-1995;
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27-FEB-1997.
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23-AUG-1995; 031033
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                                                                                                                                                                      560
                         52.8%;
larity 50.0%;
Conservative
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Pred.
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Pred. No. 4.84e+01;
                     e 57; DB 24
No. 4.84e+
Mismatches
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              DB 24; Lc..
4.84e+01;
-hes 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface; epithelial;
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                                                                                              Length 560
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RESULT 13
ID R69633;
AC R69633;
AC R69633;
AC R69633;
AC R69633;
AC R69633
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                   DNA encoding a low affinity interleukin-12 receptor - used to provide the provided and the provided the provided to suppression, e.g. to suppress graft-vs-host reaction, allograft rejection or inflammation, and to treat autoimmune conditions of inflammation, and to treat autoimmune conditions of the provided the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1994; 110657.
19-JUL-1993; US-094649.
19-JUL-1993; US-094713.
19-MAY-1994; US-248532.
(HOFF ) HOFFMANN LA ROCHE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
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WPI; 95-076349/11.
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15-FEB-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interleukin-12
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   therapeutic
660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chua AO,
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superfamily Cys52..Cys62Sw"
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618..629
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(W222SKWS)"
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'note- "conserved area of cytopiasmic tail"
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Gubler UA,
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Query Match Best Local Similarity

550

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Score 55; Pred. No.

DB 13; 7.81e+01;

Length 660;

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Query Match
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19-JUL-1993; US-094649.

19-JUL-1993; US-094713.

31-MAY-1994; US-0248532.

(HOFF ) HOFFMANN LA ROCHE &

Chizzonite RA, Chua AO, G
                                              DNA encoding a low affinity interleukin-12 receptor - used to bind or scavenge IL-12 to cause immune suppression, e.g. to suppress graft-vs-host reaction, allograft rejection or inflammation, and to treat autoimmune conditions Claim 4; Page 24-27; Slpp; English.

A cDNA library of PHA-activated peripheral blood mononuclear cells in vector pEF-BOS was screened for interleukin-12 (IL-12) receptor cDNAs by panning. An isolated cDNA was sequenced (Q83844); it encoded a 662-mmino acid low affinity IL-12 receptor (R69632). Recombinant IL-12 receptor was expressed in COS cells, and can be used for therepartic or diagnostic purposes.
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Interleukin-12 receptor; IL-12; immune suppression;
immunosuppressive; graft-yers-host reaction; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                             L5-FEB-1995
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superfamily Cys52..Cys62Sw"
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          New interleukin-12 beta-2 receptor and high binding affinity complexes - have a high affinity for interleukin-12, and are used to receptor treat autoimmune diseases S Claim 8; Page 37-41; 53pp; English.

Ruman interleukin-12 (IL-12) receptor beta-1 receptor (W12772) has a low binding affinity for IL-12, but when complexed with an IL-12 beta-2 receptor (see also W12771), forms a complex with a deduced from a cDNA clone (T59732) obtd. from human lymphoblasts. Claim 12 receptor beta-1 can be expressed on the surface of transformed host cells as a complex with co-expressed IL-12 receptor beta-2, and used in therapeutic compsns., pref. with at least 1 cytokine antagonist, to treat autoimmune dysfunctions such as rheumatoid arthritis, inflammatory bowel disease and multiple store for the surface of the surface 
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23-JUL-1996; 111807.
01-AUG-1995; US-001701
30-MAY-1996; US-018674
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Interleukin-12 beta-1 receptor; IL-12; autoimmune
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456..458
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(Cys52..Cys62SW)
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/note= "signal peptide cleavage site alternatively
follows Ala-23 ir Cys-24"
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'note= "cytokine receptor superfamily motif
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'note= "cytokine receptor superfamily motif
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Query Match
SO.9%; Score 55; DB 21; Length 662;
Best Local Similarity 53.8%; Pred. No. 7.81e+01;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db 14 lfllsrqgaacrt 26
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c):1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:32:12 1999; MasPar time 4.36 Seconds 137.938 Million cell updates/sec

Tabular output not generated.

Perfect Score: Sequence: Title: >US-08-991-628-4 (1-15) from US08991628.pep 108 1 TPMFLLSRNTGEVRT 15

scoring table:

PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Database:

Mean 27.020; Variance 36.303; scale 0.744

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22222111111111111111111111111111111111	Result No.
108 888 888 888 888 888 888 655 653 653 653 653 653 653 653 653 653	Score
100 0 781.5 80.22 80.23	Query Match
10449 10449 10449 572 2972 2972 2973 586 586 586 586 586 586 586 586 587 1102 1102 1102 1117	Length 1
222112222222222222	BB
IJHUG3 IJHUG1 IJBOG1 S55982 S552694 S32892 S5636482 AJPMN12 S69182 AJPMN12 S69183 F71058 S59183 F71058	Ü
desmoglein 3 precurso desmoglein 1 precurso desmoglein 1 precurso asparagine synthase (asparagine synthase (hypothetical protein inner membrane copper hypothetical protein asparagine synthase (guanylate cyclase (EC dual specificity phos asparagine synthase (inner membrane copper desmoglein 2 - human hypothetical protein	Description
2.99e-11 7.26e-05 7.26e-05 1.80e-01 1.47e-01 4.47e-01 1.09e+00 1.09e+00 1.09e+00 1.09e+00 1.09e+00 2.61e+00 2.61e+00 6.14e+00 6.14e+00 6.14e+00 9.34e+00	Pred. No.

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B47452	G64922	A70755	A32992	S34226	JC2555	I49008	JC2193	S37397	S16307	B60030	A71536	S36550	PQ0061	S17925	I37892	YKMY	T02000	F70952	S04671	G70785	T/OOMP
dual specificity phos	probable ATP-dependen	hypothetical protein	cyclin Bl - human	cyclin B - rat		melanocortin-5 recept	melanocortin receptor	regulatory protein fn	transcription activat	gene B protein - alce	hypothetical protein	E6 protein - human pa	T-cell receptor beta	polynucleotide adenyl	IL12 receptor compone	citrate (si)-synthase	hypothetical protein	probable corA protein	H+-transporting ATP s	hypothetical protein	asparagine synthase (
3.17e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	2.12e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	9.34e+00

ALIGNMENTS

Query Match Best Local Similarity Matches 15; Consei	937-956 937-956 110,180,545 SUMMARY	50-615 52-157 160-267 270-498 390-498 496-598 616-639 610-938	FEATURE 1-23 24-49 50-999	#gene GDB:DSG #gene GDB:DSG #gene GDB:DSG ##oross-references ##orp_position 18912.1 CLASSIFICATION #superf KEYWORDS calcium trans	#title #cross-refere #accession #molecule ##residues	RESULT 1 ENTRY TITE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE ##11+10-F5
100.0%; Score 108; DB 1; Length 999; nllarity 100.0%; Pred. No. 2.99e-11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	desmoglein repeat *label desmoglein repeat *label g_site carbohydrate (Asn) cted #molecular-weight 107502	#domain extracellular #status predicted #label EXT\ #domain extracellular #status predicted #label CR1\ #domain cadherin repeat homology #label CR2\ #domain cadherin repeat homology #label CR3\ #domain cadherin repeat homology #label CR4\ #domain cadherin repeat homology #label CR5\ #domain cadherin repeat homology #label CR5\ #domain transmembrane #status predicted #label TMM\ #domain intracellular #status predicted #label INT\ #domain desmoolein repeat #label DG1\	#domain signal sequence #status predicted #label SIG\ #domain propeptide #status predicted #label PRO\ #product desmoglein homolog #status predicted #label	GDB:DSG3 :ferences GDB:134030; OMIM:169615 :ferences GDB:134030; OMIM:169615 :ferences GDB:134030; OMIM:169615 #superfamily cadherin; cadherin repeat homology calclum binding; cell adhesion; duplication; glycoprotein; transmembrane protein	cell (1991) 67:869-877 Autoantibodies against a novel epithel pemphigus vulgaris, a disease of cel nces MUII:92069753 AA1088 Atype mRNA _type mRNA 1-999 ##label AMA ferences GB:M76482; NID:g190751; PID:g1	desmoglein 3 precursor - human pemphigus vulgaris antigen #formal_name Homo sapiens #common_name man #formal_993 #sequence_revision 30-Jun-1993 #text_change 18-Sep-1998 A41088 A41088 A41088 A41088 AMBGAI M Klaus-Kovtun V : Stanley J.R.

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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Arnemann, J.;

Rees, D.A.; King, I.A.; Magee, A.I.

#journal Biochem. Soc. Trans. (1991) 19:1060-1064

#title Desmosomal glycoproteins I, II and III: novel members of the cadherin superfamily.

#cross-references MUID:92175187
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#accession A39706
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ip_position 18q12.1-18q12.2
ip_position 18q12.1-18q12.2
firication #superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
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##residues 1-55 ##label WH3
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desmoslein 1 precursor - human
desmosomal glycoprotein I
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993
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J. Cell Sci. (1991) 99:809-821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wheeler, G.N.; Parker, A.E.; Thomas, C.L.; Ataliotis, P.; Poynter, D.; Arnemann, J.; Rutman, A.J.; Pidsley, S.C.; Watt, F.M.; Ress, D.A.; Buxton, R.S.; Magee, A.I. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800 Desmosomal 9lycoprotein DGI, a component of intercellular desmosome junctions, is related to the cadherin family cell adhesion molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S16906; A39706; A61254; A61279; S16158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, November 1990
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                                                                      #domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label PRO\
#product desmoglein #status predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR4\
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                                                        region serine/threonine-rich
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transmembrane #status predicted #label INM\ intracellular #status predicted #label INT\
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##residues 44-1043 ##label ZIM
##cross-references EMBL:X57784; NID:g436061; PID:g436062
REFERENCE A48173
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870-899
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110,180
                 #journal #title
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#title
                                                                                                                                                                                                                                                                                             #title Desmoglein shows extensive homology to the cadherin cell adhesion molecules.
#cross-references MUID:91097553
#accession A37785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal Eur. J. Cell Biol. (1991) 55:200-208
#title Complete amino acid sequence of the epidermal desmoglein
precursor polypeptide and identification of a second type
of desmoglein gene.
#cross-references MIID:92037656
                                                                                                                                                                   #accession
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                                                                       #authors
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                                                                                                                                                                                                                                       ##residues 44-123,'V',125-493 ##label ##cross-references GB:M58165; NID:g162966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
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Similarity 66.7%;
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Complete sequence of the desmoglein precursor and evidence for the existence of different desmoglein genes expressed in cell type-specific patterns.
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       Koch, P.J.; Walsh, M.J.; Schmelz, Zimbelmann, R.; Franke, W.W. Eur. J. Cell Biol. (1990) 53:1-12 Identification of desception a cc
                                                                                                                                                                                  Zimbelmann, R. submitted to the
                                                                                                                                                                                                                                                                                                                                                                                                          Goodwin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Bos primigenius taurus #common_name cattle 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. (1990) 173:1224-1230
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Pred. No. 1.87e-06;
5; Mismatches 0
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                                                                     M.J.; Schmelz, M.; Goldschmidt,
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#accession A48173
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##residues 44-1001,'AQPPSAT' ##label KO3
##cross-references GB:X57784
##note this sequence has been revised in
$38721
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                                                    ##molecule_type DNA
##molecule_type DNA
1-572 ##label VAW
                      ##cross-references EMBL:272909; NID:g1323202; PID:e243463; PID:g1323203; MIPS:YGR124w
                                                                                                                                                                                                          ##cross-references EMBL:X83099; NID:g642340; PID:g642347
##experimental_source
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                                                                                                                                                                                                                                                                                           van Dyck, L.; Goffeau, A. submitted to the EMBL Data Library, December 1994 Genes for an asn synthase, a GLFG-motif nucleoporin and a putative homeobox-domain protein are identified on a 18.3 kb segment of the yeast chromosome VII also carrying MEP1, ppT1, tree new ORFs, remnants of Ty and three tRNA genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yeast (Saccharomyces cerevisiae)
protein G6358; protein YGR124w
#formal_name Saccharomyces cerevisiae
23-aug-1995 #sequence_revision 19-Oct-1995
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calcium binding; cell adhesion;
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llarity 60.0%;
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Talla, E.;
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                                                                                                                         L.; Skala, J.; de Wergifosse, P.; Purnelle, E.; Nawrocki, A.; Del Bino, S.; Goffeau, A. to the Protein Sequence Database, May 1996
  strain
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##cross-references EMBL:U40829; NID:gl066476; PID:gl066479; MIPS:YPR145w
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Local Similarity 88.9%;
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- yeast (Saccharomyces cerevisiae)
protein P659.3; protein YRR145w
#formal_name Saccharomyces cerevisiae
19-May-1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fulton, L. submitted to the EMBL Data Library, November 1995. The sequence of S. cerevisiae cosmid 9659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, March 1995 Multiple regulatory systems control expression of the Saccharomyces cerevisiae ASN1 and ASN2 genes at the
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                                hypothetical protein 6 precursor - Salmonella typhimurium #formal_name Salmonella typhimurium 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 177Mar-1999
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#journal Mol. Microbiol. (1995) 15:1127-1137
#title Molecular genetics of a chromosomal locus involved tolerance in Escherichia coli K-12.
#cross-references MUID:95349397
                                                                                                                                                #accession
                                                                                                                                                             #authors Crooke, H.; Cole, J.
#authors Crooke, H.; Cole, J.
#journal Mol. Microbiol. (1995) 15:1139-1150
#title The biogenesis of c-type cytochromes
requires a membrane-bound protein,
disulphide isomerase-like domain.
#cross-references_MUID:95349398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-295 ##label FRI
##cross, references EMBL:L08613
# #length 295 #molecular-weight 31162 #checksum
                        ##residues 'M',78-565 ##label RE2
##cross-references EMBL:X77707; NID:9871027; PID:9871029
##note in this report, the codon GTG for Val-77
                                                                                                                                                                                                                                                                                                            ##cross-references EMBL:236905; NID:g535290; PID:g581055
##note in this report, the codon GTG for Val-77 was interpreted
as a start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
##residnes
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##residues 'M',78-565 ##label_RES
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##note the nucleotide sequence was submitted to .
                                                                                                 #molecule_type DNA
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Local Similarity 80.0%;
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Nucleic Acids Res. (1995) 23:2105-2119

Analysis of the Escherichia coli genome VI: DNA sequence the region from 92.8 through 100 minutes.

NUCLES MUID:95334362
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Nucleotide sequence of a 13 9kb segment of the 90kb virulence plasmid of Salmonella typhimurium: the presence of fimbrial biosynthetic genes.

DOES MOID:93316852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Escherichia coli
28-oct-1995 #sequence_revision 03-Nov-1995 #text_change
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0; Mismatches
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REFERENCE A64720
                                                                                 #map_position
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  Query Match 58.3%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
#accession F65223
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                                                                                                                                         ##cross-references EMBL:U18778;
                                                                                                                                                                               ##molecule_type DNA
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NCE S57220
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#length 923 #molecular-weight 103333
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submitted to the EMBL Data Library, February 1994
The biogenesis of C-type cytochromes in Escherichia col
requires an integral membrane protein with a protein
disulphide isomerase like domain.
                                                                                                                                                                                                                       submitted to the EMBL Data Library, December 1994 The sequence of S. cerevisiae cosmids 9537, 9581, and lambda clone 5898.
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inner membrane; redox-active disulfide; transmembrane protein
#length 565  #molecular-weight 61795  #checksum 2685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missiakas, D.; Schwager, F.; Raina, S.
EMBO J. (1995) 14:3415-3424
Identification and characterization of a new disulfide
isomerase-like protein (DsbD) in Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shav
                                                                                                                                                                                                      S50482
                                                                                                                                                                                                                                                                                                                                          cerevisiae)
#formal_name Saccharomyces cerevisiae
28-May-193 #sequence_revision 24-Feb-1995
21-Nov-1997
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Score 63; DB 2; I
Pred. No. 4.47e-01;
4; Mismatches 2
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#title
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#journal EMBO J. (1990) 9:323-332
#title Dark-induced and organ-specific expression of two asparagine
#tttle synthetase genes in Pisum sativum.
#cross-references MUID:90151604
                                                                                                                                                                                                                                                     #cross-references MUID:96270368
#accession S69182
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 y Match
Local Similarity 77.8%;
hes 7; Conservative
                                                                                                                                                            ##cross-references EMBL:X89409; NID:g897770; PID:g897771
##experimental_source strain B-129
                                                                                                                                                                                                   ##residues
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Similarity 77.8%;
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                                                                                                                                                                                                                                                                                    Waterhouse, R.N.; Smyth, A.J.; Massonneau, A.; Prosse Clarkson, D.T.
Plant Mol. Biol. (1996) 30:883-897
Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus: dynamics of aspara synthesis in N-sufficient conditions.
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asparagine biosynthesis; ligase
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                                                                    #superfamily asparagine synthase (glutamine-hydrolyzing)
asparagine biosynthesis; ligase
#length 586 #molecular-weight 66461 #checksum 3372
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asparagine synthase (glutamine-hydrolyzing)
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31-pec-1991 #sequence_revision 31-pec-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                               S69182; S57931
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19-Mar-1997 #sequence_revision
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th 583 #molecular-weight 65649 #checksum 2836
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2; Mismatches 0
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##cross-references EMBL:X52179; NID:g20649; PID:g20650
##cross-references EMBL:X52179; NID:g20660
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##cross-references Explix86448; ND:9669056; PID:9669057
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and a glutamine amide transfer domain, which binds glutamine
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An asparagine synthetase cDNA clone from Broccoli (Brassica
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#Journal Plant Mol. Biol. (1996) 30:883-897

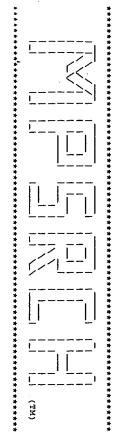
#title Molecular cloning and characterisation of asparagine synthetase from Lotus Japonicus: dynamics of asparagine synthesis in N-sufficient conditions.

#cross-references MVID:96270368
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##cross-references EMBL.X89410; NID:g897772; PID:g897773
##experimental_source strain B-129
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#formal_name Lotus japonicus
19-Mar-1997 #sequence_revision 19-Mar-1997
08-Sep-1997
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Metabolic regulation of asparagine synthetase gene expression in maize (Zeamays L.) root tips.
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 1 TPMFLLSRN 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||:||:
1 TPMFLLSRN 9
                                                                                                                                                                                                                                                    Yamaya, T.; Higuchi, T. submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                         T03602
                                                                                                                                                                                                                                                                                                                                                                                probable asparagine synthase (glutamine-hydrolyzing) (EC
                                                                                                                                                                                                                                                                                                                               #formal_name Oryza sativa #common_name rice 24-Mar-1999 #sequence_revision 24-Mar-1999 #
                                                               Conservative
                                                                                                                                                                                                                                                                                        Z14971
                                                                                                                                                                                         1-591 ##label YAM
                                                                                                                                                                                                                       preliminary; translated from GB/EMBL/DDBJ
                                                                            56.5%;
                                                            Score 61; DB 2; I
Pred. No. 1.09e+00;
2; Mismatches 0
                                                                                         Length 591
                                                               Indels
                                                               0
                                                               Gaps
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:29:22 1999; MasPar time 2.45 Seconds 172.912 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score: Title: >US-08-991-628-4 (1-15) from US08991628.pep 108 1 TPMFLLSRNTGEVRT 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 27.687; Variance 32.651; scale 0.848

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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222	20	15 17 15	13	110	voα	76	∪: 4	ω 2		Result No.
57 57	រៈ ភេ <i>ភ</i> ភូមូ ម	ខ្លួញ	61	ខ្ម	61 61	63 3	0 0 5 5	88 81	108	Score
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554 579 1117	589 1103	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	585 585	583 585	524 582	488 923	571 571	1049 1043	666	% Query Match Length
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ASNB_ECOLI DSBD_HAEIN DSG2_HUMAN	CYGD_HUMAN	ASN1_PEA ASN1_LOTJA ASNS_ORYSA	ASNS_BRAOL ASNS_MAIZE ASN2_LOTJA	ASNS_ARATH ASNS_TRIVS	ASNS_SANAU ASN2_PEA	YEL4_YEAST	ASN1_YEAST ASN2_YEAST	DSG1_HUMAN DSG1_BOVIN	DSG3_HUMAN	ID
() H ()	ASPARAGINE SYNTHASE [G RETINAL GUANYLYL CYCLA		ASPARAGINE SYNTHETASE ASPARAGINE SYNTHETASE ASPARAGINE SYNTHETASE		ASPARAGINE SYNTHETASE,	THIOL: DISULFIDE INTERCHE HYPOTHETICAL 103.3 KD	ASPARAGINE SYNTHETASE	ىر بر	DESMOGLEIN 3 PRECURSOR	Description
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44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
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49.1	49.1	49.1	49.1	49.1	49.1	•	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.9	50.9	50.9	50.9
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YLW5_CAEEL FAT_DROME	VIB4_AGRT5	KP78_HUMAN	Y306_MYCPN	MURB_MYCTU	MC5R_BOVIN	LHR_ECOLI	Y089_MYCTU	CGB1_HUMAN	CGB1_MESAU	CGB1_RAT	FD3E_TOBAC	MC5R_MOUSE	MC5R_RAT	FNRA_PSEST	ANR_PSEAE	VE6_HPV03	I12R_HUMAN	CISY_MYCSM	ATPD_RHOBL	YOOH_MYCTU
HYPOTHETICAL 105.9 KD CADHERIN-RELATED TUMOR	VIRB4 PROTEIN PRECURSO	PUTATIVE SERINE/THREON	HYPOTHETICAL PROTEIN M	PUTATIVE UDP-N-ACETYLE	MELANOCORTIN-5 RECEPTO	PROBABLE ATP-DEPENDENT	HYPOTHETICAL ABC TRANS	G2/MITOTIC-SPECIFIC CY	G2/MITOTIC-SPECIFIC CY	G2/MITOTIC-SPECIFIC CY	OMEGA-3 FATTY ACID DES	MELANOCORTIN-5 RECEPTO	MELANOCORTIN-5 RECEPTO	TRANSCRIPTIONAL ACTIVA	TRANSCRIPTIONAL ACTIVA	E6 PROTEIN.	INTERLEUKIN-12 RECEPTO	CITRATE SYNTHASE (EC 4	ATP SYNTHASE DELTA CHA	VERY HYPOTHETICAL 14.0
1.28e+01 1.28e+01	1.28e+01	1.28e+01	1.28e+01	1.28e+01	1.28e+01	8.22e+00	8.22e+00	5.24e+00	5.24e+00	5.24e+00	5.24e+00									

ALIGNMENTS

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M76482; G190752; A41088; IJHUG3. 169915; TE: PS00232; CADHERIN; 3. PF00028; cadherin; 4. P09803; IEDH.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).	VULGARIS (PV) IS A POTENTIALLY IDERMAL BLISTERS OCCUR AS THE F DHESION CAUSED BY THE ACTION OF TO THE CADHERIN FAMILY. BELONGY.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 92069753. AMAGAI M., KLAUS-KOVTUN V., STANLEY J.R.; PANTOANTIBODIES against a novel epithelial cadherin in pemphigus PULIGATIS, a disease of cell adhesion."; CELL 67:869-877(1991). -!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. -!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND CARCINOMAS. -!- TOSUBLICITY MAY BE BOUND BY THE CADHERIN-LIKE REPEATS	LT 1 DSG3_HUMAN STANDARD; PRT; 999 AA. P32926; O1-OCT-1993 (REL. 27, CREATED) O1-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DESMOGLEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA). DSG3. HOMO SAPIENS (HUMAN). BUGARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                               ARNEMANN J., RUTMAN A.J., P
BUXTON R.S., MAGEE A.I.;
"Desmosomal glycoprotein DG
junctions, is related to th
molecules.";
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01-OCT-1993
01-NOV-1997
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SEQUENCE
                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                          PROC. NATL. ACAD. SCI. U.S.A. 88:4796-4800(1991).
-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDI
FILAMENTS MEDIATING CELL-CELL ADDESION.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND OESOPHAGUS.
-!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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                                                   or send an
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                                                                                                                                        (POTENTIAL).
SIMILARITY: BELONGS TO
                                                                                                                                 DESMOSOMAL SUBFAMILY
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             ; X56654; G30506;
S16906; IJHUG1.
125670; -.
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Similarity 100.0%;
15; Conservet'
                                                              requires a license agreement
   PS00232; CADHERIN;
                                                   email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     (REL.
                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR
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LAST SEQ
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LAST ANNOTATION UPDATE)

(DESMOSOMAL GLYCOPROTEIN 1)
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                                                                                                                                                                                                                                                                       PIDSLEY S.C.,
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                                                                                                                                           THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
DESMOGLEIN 3.
EXTRACELLULAR (
POTENTIAL.
CYTOPLASMIC (PO
CADHERIN 1.
   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108; DB 1;
Pred. No. 4.34e-13;
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DESMOGLEIN
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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CADHERIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            1049
                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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AND INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                          (DG1).
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Best Local S
Matches
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                                                                             REVISIONS, AND SEQ
MEDLINE; 92037656.
KOCH P.J., GOLDSCH
FRANKE W.W.;
                                                 "Complete amino a
polypeptide and i
EUR. J. CELL BIOI
                                                                                                                                                                                                                                                                                                                       01-OCT-1993
01-OCT-1993
01-NOV-1997
DESMOGLEIN 1
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CARBOHYD
CARBOHYD
CARBOHYD
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REPEAT
SEQUENCE OF 44-493 FROM N.A.
MEDLINE; 91097553.
GOODWIN L., HILL J.E., RAYNOR K., RAS
"Desmoglein shows extensive homology
                                                                                                                                                         MEDLINE; 91168965.

KOCH P.J., WALSH M.J., SCHM
ZIMBELMANN R., FRANKE W.W.;
"Identification of desmogle
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D., ZIMBELMANN R., FRANKE W.W.;
SUBMITTED (MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                          glycoprotein, as a
molecules.";
                                                                                                                                                                                                   SEQUENCE OF 44-1043 FROM TISSUE-MUZZLE EPITHELIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                              EUR. J. CELL BIOL.
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                                                                                                                                                                                                                                                                                                                                                                                                                1 TPMFLLSRNTGEVRT
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                                                                                                                                                                                                                                                                        (BOVINE).
METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
LA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE
                                                                                                                                                                                                                                                                                                                        1 PRECURSOR
                                                                                        GOLDSCHMIDT M.D.,
                                                                                                                                                                                                                                                                                                                                 (REL.
                                                 BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                           SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                 acid sequence of the identification of a s OL. 55:200-208(1991).
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27, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE
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Pred. No.
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                                                                                                                                                  constitutive desmosomal cadherin family of cell
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 RASZI
ogy to
                                                                                                                                                                               GOLDSCHMIDT M.D.
                                                          e epidermal desmoglein precursor
second type of desmoglein gene.";
                                                                                                                                                                                                                                                                                                                                                                          1043 AA
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 the
                                                                                        ZIMBELMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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MANABE M., COWIN P.; cadherin family of c
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Matches
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CARBOHYD
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CONFLICT
                                                  AT 4
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949089;
P49089;
O1-FEB-1996 (REL. 33, CREATED)
O1-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
O1-OV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
ASPARAGINE-DEPENDENT ASPARAGINE SYNTHETASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X58466; G307; -. EMBL; X57784; G436062; -. EMBL; M58165; G552318; -. PIR; S14603; IJBOG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                    ASN1 OR YPR145W OR P9659.3.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALCIUM-BINDING; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S14603; IJBOG1.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adhesion molecules.";
BIOCHEM. BIOPHYS. RES.
                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                     206 SPMFIINRYTGEIRT
                                                                                                                                                                                                                       Local Similarity
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE
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                                                                                                                                                                                                            Conservative
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DESMOGLEIN REPEAT 3
DESMOGLEIN REPEAT 4
DESMOGLEIN REPEAT 4
DESMOGLEIN REPEAT 5
GLY/SER-RICH.
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                                                                                                                                                                                                          Score 81; DB 1; I
Pred. No. 6.60e-06;
5; Mismatches 1
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POTENTIAL.
DESMOGLEIN 1.
EXTRACELLULAR (
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CADHERIN
CADHERIN
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CYTOPLASMIC
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13898584 CRC32;
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ng as its content
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                      SACCHAROMYCETALES
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A FAVELLO A., FULTON L., GARTUNG S., GRECO T., KIRSTEN J., KUCABA 1
A HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
A JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZEN
A MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
A MILLER N., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUD:
A WILSON R., WATERSTON R.,
I SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
C -1- CATALTYIC ACTIVITY: ATP + L-ASPARRATE + L-GLUTAMINE - AMP +
C PYROPHOSPHATE + L-ASPARRATINE + L-GLUTAMINE - AMP +
C -1- PATHWAY: ASPARRAGINE BIOSYNTHESIS.
C -1- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                         SULT 5
ASN2_YEAST STANDARD; PRT; 571 AA.
P49090;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] 2 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 2).
ASPARAGINE SYNTHETASE (BAKER'S YEAST).
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
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FAVELLO A., FULTON L., GAT
HALLSWORTH K., HAWKINS J
JOHNSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MULTIGENE
INIT_MET
ACT_SITE
                                                                                                                 SEQUENCE FROM N.A.
STRAIN-5288C / FY1679;
MEDLINE; 97197982
VAN DYCK L., TETTELIN H., PURN
"An 18.3 kb DNA fragment from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                              unknown open reading frames, of Ty and three trnA genes."; YEAST 13:171-176(1997).
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DANG V.D., BOLOTIN-FUKUHARA M., DAIGNAN-FORNIER
SEQUENCE FROM
                                                                                                                                                                                                                                                                       SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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PFAM; PF00310; GAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO OTHER ASN SYNTHETASES.
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Asn_synthase; 1.
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                                                                                                                                              PURNELLE B.,
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Pred. No.
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No. 4.12e-02;
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VII carries
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L outstation -
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RESULT AND SERVICE SERVICES OF SERVICES OF
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Best Local
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P36655; P76796;

01-JUN-1994 (REL. 29, CREATED)

01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

THIOL:DISULFIDE INTERCHANGE PROTEIN DSBD (C-TYPE CYTOCHROME BIOGENESIS PROTEIN CYC2) (INNER MEMBRANE COPPER TOLERANCE PF DSBD OR CYC2 OR CUTA2 OR DIPZ.

ESCHERICHIA COLI.

ESCHERICHIA COLI.

BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIA;
                                                                                                                                                                                                                                                                MEDLINE; 95349397.
FONG S.-T., CAMAKARIS
SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 95334362.
BURLAND V.D., PLUNKET
                                                                                                                                                                                                                                                                                                                                                                                                                                          CROOKE H., COLE J.;
The biogenesis of c-type cytochromes
"The biogenesis of c-type cytochromes
membrane-bound protein, DipZ, with a promerase-like domain.";
somerase-like domain.";
MICROBIOL. 15:1139-1150(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE
-YROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
-I- PATHMAY: ASPARAGINE BIOSYMTHESIS.
-I- STMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INIT_MET ACT_SITE
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EMBL; Z72909; E243463; -.
SGD; L0003156; ASN2.
PROSITE; P800443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                     FONG S.-T., CAMAKARIS J., LEE B.T.O.;
"MOLECULAR genetics of a chromosomal
tolerance in Escherichia coli K-12.";
MOL. MICROBIOL. 15:1127-1137(1995).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-K12 / W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12;
MEDLINE; 95349398.
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PF00733; ASG_SYNTHASS; 1.
E; ASPARAGINE BIOSYNTHESIS; GLUTAMINE AMIDOTRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 88.9% 8; Conservative
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   PLUNKETT
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88.9%;
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   III,
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Pred. No. 4.12e-02;
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GATASE (BY SIMILARITY).
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   SOFIA H.J.,
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   DANIELS
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MBL outstation -
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EMBL; U14003; G536980; ALT_
EMBL; AE000486; G1790578; A
EMBL; Z36905; G581055; -
PIR; S42064; S42064.
                                                                                                                                         TRANSMEM DOMAIN DISULFID CONFLICT SEQUENCE
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as 
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SAMBONGI Y., FERGUSON S.J.;

SOPECIFIC TAILOR OF A COMPOUNT AND A 
                                                                                                                                                                                                                                                                TRANSMEM DOMAIN
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TRANSMEM
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"Analysis of the Escherichia coli genome region from 92.8 through 100 minutes.";

NUCLEIC ACIDS RES. 23:2105-2119(1995).
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MISSIAKAS D., HUGHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSIAKAS
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                                        Similarity. 53.8%
7; Conservative
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PS00194; THIOREDOXIN;
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No. 1.14e-01
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DIETRICH F.S., MULLIAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,
AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.
CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICKE-SMITH S.,
HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,
MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH C.,
PETEL F.X., ROBERTS D., SEHL P., SCHRAMY S., SHOGREN T., SMITH V.,
TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (REL. 31
01-FEB-1995 (REL. 31
01-FEB-1995 (REL. 31
HYPOTHETICAL 103.3 P
                                                                                                                                                                                                                                                                                                          ASNS_SANAU STANDARD; PRT; 524 AA. 024338; 15-DEC-1998 (REL. 37, CREATED) 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) ASPARACINE SYNTHETASE (GLUTAMINE-HYDROLYZING) DEPENDENT ASPARAGINE SYNTHETASE).
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P40017;
EASON J.R., KING G.A.;
"Nucleotide sequence of cDNA encoding
Sandersonia aurantiaca.";
(IN) PLANT GENE REGISTER PGR97-112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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PROSITE; PS00440; ACYLTRANSF_C_2; 1
PFAM; PF00755; Carn_acyltransf; 1.
HYPOTHETICAL PROTEIN; TRANSFERASE;
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                                                                                                                                                                                                                        EUPHYLLOPHYTES;
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EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMY
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                                                                                                                                          SEQUENCE FROM N.A.
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31, LAST SEQUENCE UPDATE)
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31, LAST ANNOTATION UPDATE)
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Pred. No. 1.14e-01
4; Mismatches
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                                                                                                                                                                                                                                                EMBRYOPHYTA;
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EMBRYOPHYTA; TRACHEOPHYTA;
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Best Local Similarity
Matches 7; Consei
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ACT_SITE
SEQUENCE
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P19252;
                                                                                                                                                                         "Dark-induced and organ-specific expression of two synthetase genes in Pisum sativum.";
EMBO J. 9:323-332(1990).
-i- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTA PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
                                                                                                                                                                                                                                     MEDLINE;
TSAI F.Y.
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (REL. 16, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE, ROOT [GLUTAMINE-HYDROLYZING]
(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE).
                                                                               This
                                                                                                                                                                                                                                                                                                           PISUM SATIVUM (GARDEN PEA).
EUKARYOTA; VIRIDIPLANTAE; STREI
EUPHYLLOPHYTES; SPERMATOPHYTA;
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PROSITE; PS00443; GATASE_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                 INDUCTION: DARK-INDUCED. SIMILARITY: THE GATASE I AMIDOTRANSFERASES.
                                                                                                                                                    PATHWAY: ASPARAGINE BIOSYNTHESIS TISSUE SPECIFICITY: ROOTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYROPHOSPHATE + L-ASPARAGINE + L-PATHWAY: ASPARAGINE BIOSYNTHESIS
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                                                                                                      SIMILARITY: TO OTHER ASN SYNTHETASES.
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                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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PF00733; Asn_syntha
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                                                                                                                                                                                                                                                              SPARKLE;
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SPARAGINE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                        STREPTOPHYTA;
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Pred.
2; M
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PHYTA; EUDICOTYLEDONS; ROSI
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There are no restrictions ong as its content is in

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PROSITE; PS00443; GATASE_TYPE_II;

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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
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EUKARXOTA; VIRIDIPLANTAE; STREPTOPHYTA; EUBRYOPHYTA; TRACHEOPHYTA;
EUPRYLLOPHYTES; SPERNATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                              MULTIGENE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 TPMFLMSRK 329
                       321 TPMFLMSRK 329
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L29083; G507946; -
                                                                                                                                                                                                                                                      ASPARAGINE BIOSYNTHESIS; GLUTAMINE AMIDOTRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
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2; Misma
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Pred. No. 3.06e-01;
2; Mismatches 0
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GATASE (BY SIMILA
793421FA CRC32;
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GATASE (BY SI
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                                                                                                                                                           ATASE (BY
F8FC9672
                                                                     Mismatches
                                                                                          No. 3
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                                                                                                              DB 1;
                                                                                                                                                           SIMILARITY).
CRC32;
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                                                                                                           Length 583;
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                                                                  Indels
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Best Local Similarity
Matches 7; Conse
                                                                                                              ASNS_BRAOL STANDARD; PRT; 585 AA.
P49091;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
DEPENDENT ASPARAGINE SYNTHETASE).
BRASSICA OLERACEA (CAULLIFLOWER).
BRASSICA OLERACEA (CAULLIFLOWER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Host root exudate increases expression of asparagine synthetase the roots of a hemiparasitic plant Triphysaria (Scrophulariaceae) SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE = AMP + PATHANATE + L-SPARAGINE + L-GLUTAMATE.

-I- PATHANX: ASPARAGINE BIOSYNTHESIS.

-I- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRIPHYSARIA VERSICOLOR.
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA;
TRACHEOPHYTA; EUPHYLLOPHYTES; SPERWATOPHYTA; MAGNOLIOPHYTA;
EUDICOTYLEDONS; ASTERIDAE; GENTIANANAE; LAMIALES; SCROPHULARIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF014055; G2429280; -.
EMBL; AF014055; G2429282; -.
EMBL; AF014057; G2429284; -.
PROSITE; PS00443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEPENDENT ASPARAGINE SYNTHETASE).
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15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            024661;
                                                                             EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRY. EUPHYLLOPHYTES; SÆRMATOPHYTA; MAGNOLIOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (s or send an email to license@isb-sib.ch).
  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00310; GATase_2; 1.
PFAM; PF00733; Asn_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L5-DEC-1998
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SIMILARITY: TO OTHER ASN SYNTHETASES.
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0 BY SIMILARITY.
1 GATASE (BY SIMILARITY).
65560 MW; B3ACC66E CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61;
Pred. No.
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3.06e-01
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                                                                                                           EMBRYOPHYTA;
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                                                                               EUDICOTYLEDONS;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                      "Metabolic regulation of asparagine synthetase gene expres maize (Zea mays L.) root tips.";
PLANT J. 9:1-11(1996)
-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE =
PYROPHOSPHATE + L-ASPARACINE + L-GLUTAMATE.
-I- PATHWAY: ASPARACINE BIOSYNTHESIS.
-I- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAM AMIDOTRANSFERASES.
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ACT_SITE
SEQUENCE
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X84448; G669057; -
PROSITE; PS00443; GATASE_TYPE_II; 1.
PFAM; PF007310; GATASE_2; 1.
PFAM; PF00733; Asn_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. DEA; TISSUE-ROOT MEDLINE; 96158342.
CHEVALIER C., BOURGEOIS E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>'</del>-
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DOWNS C.G., POGSON B.J., DAVIES K.M., ALMIRA E.C.;
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
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EURARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA.
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASNS_MAIZE P49094;
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O BY SIMILARITY.

ACT_SITE 1 1 GATASE (BY SIMILARITY).

SEQUENCE 585 AA; 65541 MW; B6DCFB50 CRC32;
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-!- CATALYTIC ACTIVITY: ATP + L-ASI
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                                                                                                                                                                                                                                                                                                                             <del>-</del>
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PATHWAY: ASPARAGINE BIOSYNTHESIS.
SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAM
                                                                                                                                                                                                                                                                                            SIMILARITY: TO OTHER ASN SYNTHETASES.
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larity 77.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-ROOT MERISTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61;
Pred. No.
2; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUST D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , RAYMOND P.;
synthetase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585
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편
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                                                                                                                                                                                                                                                                                                                                                                                                        GLUTAMINE
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STINKER REPORTED BY A COLOR CO
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Best Local
Ouery Match 56.58
Best Local Similarity 77.88
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASN2_LOTJA STANDARD; PRT; 585 AA. P49093; 01-FEB-1996 (REL. 33, CREATED) 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE) 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X82849; G984262; -.
MAIZEDB; 79071; -.
PROSITE; PS00443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conditions.";

PLANT MOL. BIOL. 30:883-897(1996).

-i- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE =

PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                            PFAM; PF00310; GATase_2; 1.
PFAM; PF00733; Asn_synthase; 1.
HSSP; P17169; IGMS.
LIGASE; ASPARAGINE BIOSYNTHESIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X89410; G897773; -.
PROSITE; PS00443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. GIFU / B-129;
MEDLINE; 96270368.
WATERHOUSE R.N., SMYTH A.J.,
CLARKSON D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIFABALES; FABACEAE; PAPILIONOIDEAE; LOTUS.
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO OTHER ASN SYNTHETASES.

    -!- PATHWAY: ASPARAGINE BIOSYNTHESIS.
    -!- SIMILARITY: THE GATASE DOMAIN BELONGS
    AMIDOTRANSFERASES

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular cloning and characterisation by Japonicus: dynamics of asparagine
                                                                                                                                                                                                                                                                                    MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTUS JAPONICUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPMFLLSRN
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                                                                                                                                                            585 AA;
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77.8%;
                                         56.5%;
77.8%;
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                                                                                                                                                                    Œ;
    Score 61; DB 1; I
Pred. No. 3.06e-01;
2; Mismatches C
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Pred. No. 3.06e-01;
2; Mismatches 0
                                                                                                                                                            BY SIMILARITY.
GATASE (BY SIMILARITY)
, 2FE40574 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASSONEAU
                                                                                                                                                                                                                                                                                                                         GLUTAMINE AMIDOTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A., PROSSER I.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of asparagine synthesis in N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO TYPE-2 GLUTAMINE
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                                                                              Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3.5
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Indels

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STTENER REPRESENTATION OF THE STREET 
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Search completed: Fri Jun 11 17:29:30 1999 Job time : 8 secs.
                                                                                                                                                                                                                                                              Query Match 56.5%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        MULTIGENE I
INIT_MET
ACT_SITE `
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 15
479251;
PRT; 585 AA.
P19251;
P1900 (REL. 16, CREATED)
O1-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE, NODULE [GLUTAMINE-HYDROLYZING] (EC. 6.3.5.4)
ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X52179; G20650; -.
PIR; S11444; AJPMN1
PROSITE; PS00443; GATASE_TYPE_II; 1.
PFAM; PF00310; GATASE_2; 1.
PFAM; PF00733; ASn_synthase; 1.
HSSP; P17169; IGMS.
LIGASE; ASPARAGINE BIOSYNTHESIS; GLUTAMINE AMIDOTRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Dark-induced and organ-specific expression of two asparagine synthetase genes in Pisum sativum.";

EMBO J. 9:323-332(1990).

-i-CATALUTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE = AMP + PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.

-i- PATHWAY: ASPARAGINE BIOSYNTHESIS.

-i- TISSUE SPECIFICITY: NODULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. SPARKLE; TISSUE-ROOT NODULES;
MEDLINE; 90151604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PISUM SATIVUM (GARDEN PEA).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHÉOPHYTA;
EUPHYLLOPHYTES; SPERWATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; PISUM.
                                                                                                                               322 TPMFLMSRK 330
|||||:||:
1 TPMFLLSRN 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAI F.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 TPMFLMSRK 329
||||:||:
| TPMFLLSRN 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1- SIMILARITY: TO OTHER ASN SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDUCTION: DARK-INDUCED.
SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORUZZI G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                           66222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 د
                                                                                                                                                                                                                                                                 Score 61; DB 1; Length 585; Pred. No. 3.06e-01; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
GATASE (BY SIMILARITY).
; 9AB4FBC5 CRC32;
                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                     0
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******** (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run òn: Fri Jun 11 17:29:48.1999; MasPar time 6.28 Seconds 130.422 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score: >US-08-991-628-4 (1-15) from US08991628.pep 108 1 TPMFLICENTERS

Scoring table:

PAM 150 Gap 15

Searched: 179066 segs, 54579741 residues

post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 27.267; Variance 32.331; scale 0.843

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 110 110 110 110 110 110 110 110 110	Result
55 55 55 55 55 55 55 55 55 55 55 55 55	Score
\$	Query Match 1
993 11 336 2291 2 2291 2 322 3 587 10 586 10	Length DB
1 035902 2 Q04824 2 Q04824 5 Q20732 3 Q42902 3 Q42902 0 Q4329 0 Q4328 0 Q40328 0 Q40328 1 O58871 1 O58871 1 O58871 1 O58705 2 O69775 2 O69775	B ID
DESMOGLEIN 3 (FRAGMENT HYPOTHETICAL 37.7 KD PORF6 PROTEIN PRECURSOR F53H10.1. ASPARAGINE SYNTHETASE. FIBONUCLEOTIDE REDUCTA KIAA0327 PROTEIN. RIBONUCLEOTIDE REDUCTA P54 PROTEIN. RIBONUCLEOTIDE REDUCTA P54 PROTEIN. ASPARAGINE SYNTHETASE ASPARAGINE SYNTHETASE ASPARAGINE SYNTHETASE PUTATIVE MAGNESIUM AND ZNR-1.	Description
5.59e 08 3.35e 01 5.50e 01 5.50e 01 5.50e 01 5.50e 01 5.50e 01 6.05e 00 9.59e 00 9.59e 00 9.59e 00	Pred. No.

4 . U	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	
52	53	5 3	5 3	53	53	53	53	53	53	53	53	53	53	54	54	54	54	54	54	54	54	54	54	Ü
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326	1607	1468	1220	1163	814	736	578	453	433	393	373	319	215	1919	1807	792	762	610	309	244	244	170	163	oto
v	տ	N	13	տ	10	N	N	u	14	2	N	2	ഗ	w	ω	4	N	υı	ທ	้ผ	N	σ	N	
Q18666	Q94599	067762	Q98864	018820	064681	024816	P72723	Q22370	041107	008395	Q49979	086864	044017	042998	013661	075278	P96793	077330	001259	085222	Q44500	Q29035	084262	0/32/3
C47D12.3 PROTEIN.	LCFACAS5.	RNA POLYMERASE BETA SU	PATCHED PROTEIN.	SIMILARITY TO INSULIN	F22013.35.	POLYPHOSPHATE KINASE.	POTENTIAL FMN-PROTEIN.	T10B10.2 PROTEIN.	A625R PROTEIN.	CITRATE SYNTHASE (EC 4	CORA.	STRT.	ERD2 GENE.	HYPOTHETICAL 217.7 KD	HYPOTHETICAL 229.9KD P	KIAA0345-LIKE 2.	XYLQ.	MAL3P3.14 PROTEIN.	T20D3.8 PROTEIN.	ANAEROBIC REGULATORY P	CYTOCHROME BD.	CYCLIN B (FRAGMENT).	HYPOTHETICAL 18.9 KD P	カトがかくしまし、 ヒトラセ し・
3.67e+0	2.36e+0	2.36e+01	2.36e+0	2.36e+0	2.36e+01	•				2.36e+0	2.36e+01				1.51e+01		1.51e+01	1.51e+0	1.51e+01	1.51e+01	1.51e+01	1.51e+01	1.51e+01	

ALIGNMENTS

RESULTION AND COLORS CO.	Db Ma	SE S	RESULT ID O AC O DT O DT O O O O O O O O O O O O O O O
LTT 2 Q09661 Q09661; Q09661; Q09661; Q09661; Q1. NOV-1996 (TREMBLREL. 01, CREATED) Q1. NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1. NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE) Q1. NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) Q1. NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1. NOV-1996 (TREMBLREL. 01, CREATED) Q1. NOV-1996 (TREMBLEL. 01, CREATED) Q1. NOV-1996 (TREMBLREL. 01, CREATED) Q1. NOV-1996 (TREMBLEL. 01,	Query Match 83.3%; Score 90; DB 11; Length 993; Best Local Similarity 85.7%; Pred. No. 5.59e-08; Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0; 207 SMFLISRNTGEVRT 220 : : 2 PMFLLSRNTGEVRT 15	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-BALB/C; ISHIKAWA H., LI K., UITTO J.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY). EMBL; U86016; G2290200; PROSITE; PS000332; CADHERIN; 2. PFAM; PF00028; Cadherin; 4. CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT. NON_TER 993 993 SEQUENCE 993 AA; 107888 MW; 881794BD CRC32;	O35902 PRELIMINARY; PRT; 993 AA. O35902; (TREMBLREL 05, CREATED) O1-JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE) O1-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE) DESMOGLEIN 3 (FRAGMENT). DESMOGLEIN 3 (FRAGMENT). DESMOGLEIN 3 (FRAGMENT). BCS. MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.

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PART RESULT
ACSULT 4

ID 20732:
AC 202732:
DT 01-NOV-1996 (
CAENORHABDITH (
CAENORHAB (
CAENO
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Best Local
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Q04824 PREMBLREL 01, C
01-NOV-1996 (TREMBLREL 01, L
01-JAN-1999 (TREMBLREL 09, L
01-JAN-1999 (TREMBLREL 09, L
0RF6 PROTEIN PRECURSOR.
SALMONELLA TYPHIMURIUM.
PLASMID 90 KB VIRULENCE.
PLASMID 90 KB VIRULENCE.
BACTERIA; PROTEOBACTERIA; GAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-LT2;
MEDLINE; 93316852.
FRIEDRICH M.J., KINSEY N.E., VILA J
"Nucleotide sequence of a 13.9 kb s
plasmid of Salmonella typhimurium:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA
-!- SIMILARITY: WEAK, TO YEAST PROTEIN CDC20.
EMBL; 021321; G687854; -.
WORMPEP; ZX177-6; CE022095.
PFAM; PF00400; G-beta; 1.
HYPOTHETICAL PROTEIN.
SEQUENCE 336 AA; 37668 MW; 2DC77B26 CRC32;
                                                                                                                                                CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
PRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biosynthetic genes.";
MOL. MICROBIOL. 8:543-558(1993).
EMBL; L08613; G154246; -.
  SEQUENCE FROM N.A MEDLINE; 94150718
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                               J.;
(JUL-1996)
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6 (TREMBLREL. 01,
8 (TREMBLREL. 08,
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291 (
30683 MW;
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57.1%;
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                                                               EMBL/GENBANK/DDBJ
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                                                                                                                                              DDA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIDA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.03e-01;
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Pred. No. 1.22e-01;
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ORF6 PROTEIN.
; C4D5ADDF CRC32;
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                                                               DATA
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elegans.";
NATURE 368:32-38(1994).
EMBL; 277664; E255929; -.
PFAM; PF00092; vwa; 1.
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BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONHAMMER E., STALEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VAUGHAN R., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                  LT 6
P93167
                                                                                                                      GLYCINE MAX (SOYBEAN).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHEUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
                                                                                                                                                                                                                01-MAY-1997 (TREMBLREL. 03, CREATED) .
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
01-JAN-1999 (TREMBLEEL. 09, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE 2 (EC 6.3-5.4) (ASPARAGINE SY
(GLUTAMINE-HYDROLYSING)) (ASPARAGINE SYNTHETASE
(GLUTAMINE-HYDROLYSING)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SEQUENCE FROM N.A. STRAIN-CENTURY; TISSUE-MATURE LEAF MEDLINE; 97188563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-972H-;
WOOD V., RAJANDREAM M.A., BARRELL B.G., SKELTON J.,
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANK
EMBL; AL022117; E1263968; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
ASPARAGINE SYNTHETASE.
                                                                                                 FABALES; FABACEAE;
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larity 77.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61; DB 3; Leny Pred. No. 5.50e-01;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 3.35e-01;
2; Mismatches 4
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                                                                                                 GLYCINE.
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                                                                                                                                                  TRACHEOPHYTA;
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                                                                                                                           ROSIDAE;
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Best Local :
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024483;
01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL. ASPARAGINE SYNTHETASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-ROOT NODULE;
KIM H.-B., AN C.-S.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF061740; G3133675; -.
EMBL; AF061740; G313675; -.
EMBL; AF061740; -.

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065329;
01-AUG-1998
01-AUG-1998
01-AUG-1998
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an asparagine synthetase gene showing nodules and dark-adapted leaves."; PLANT CELL 9:1339-1356(1997).
EMBL; U89923; G252320; -..
PFAM; PF00310; GATASe_2; 1.
                                                                                                                     SHI L., TWARY S.N., YOSHIOKA H., GREGERSON R.G., MILLER S.S., SAMAC D.A., GANTT J.S., UNKEFER P.J., VANCE C.P.; "Nitrogen assimilation in alfalfa: isolation and characterization an asparagine synthetase gene showing enhanced expression in root
                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 97432147.
                                                                                                                                                                                                                                                                                                                                                                   MEDICAGO SATIVA (ALFALFA).
EUKARYOTA; VIRIDIPLANTAE; STRE
EUPHYLLOPHYTES; SPERMATOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELAEAGNUS UMBELLATA.
EUKARYOTA; VIRIDIPLANTAE; STRE
EUPHYLLOPHYTES; SPERMATOPHYTA;
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"Molecular cloning and expression of two cDNA

"withetase in soybean.";

PLANT MOL. BIOL. 33:301-311(1997).

-i- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L

DIPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                             FABALES; FABACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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98 (TREMBLREL.
98 (TREMBLREL.
E SYNTHETASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                      LANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOP; ERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; PAPILIONOIDEAE; MEDICAGO.
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77.8%;
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Pred. No.
2; Misma
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Pred. No.
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No. 5.50e-01
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5.50e-01;
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Q40328;
                                                                                                                                              GANTT S.;
SUBMITTED
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1819864
193618;
                                                                                                     EMBL;
PFAM;
                                                                                                                                                                                                                                                 ASPARAGINE SYNTHETASE.
MEDICAGO SATIVA (ALFALFA).
EUKARYOTA; VIRIDIPLANTAE; STREPTOP;
EUPHYLLOPHYTES; SPERWATOPHYTA; MAGI
FABALES; FABACEAE; PAPILIONOIDEAE;
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SEQUENCE
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STRAIN-KLEINE THEERINGER; TISSUE-ROOT NODULE;
STRAIN-KLEINE THEERINGER; TISSUE-ROOT NODULE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TREMBLREL, 03, CREATED)
01-MAY-1997 (TREMBLREL, 03, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL, 09, LAST ANNOTATION UPDATE)
01-JAN-1999 (TREMBLREL, 09, LAST ANNOTATION UPDATE)
ASPARAGINE SYNTHETASE (EC 6.3.5.4) (ASPARAGINE SYNTHASE
(GLUTAMINE-HYDROLYSING)) (ASPARAGINE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; VIRIDIPLANTÀE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIFABALES; FABACEAE; PAPILIONOIDEAE; VICIA.
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SEQUENCE 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUESTER H., ALBUS U., FRUEH: PUEHLER A., PERLICK A.M.; PLANT SCI. 124:89-95(1997).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
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|||||:||:
1 TPMFLLSRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 TPMFLMSRK 331
Match
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                                   ITTED (FEB-1996) TO EMBL/GE:
,; 140327; G1184265; -.
;; PF00310; GATAse=_2; 1.
;; PF00733, Asn_synthase; 1.
EL; 9036; MEDSa;1044;1.
JENCE: 586 AA; 66462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00733;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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.58;
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E + L-GLUTAMATE.
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                                         962C3A3F CRC32;
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05887];
01-AUG-1998 (TREMBLREL. 07
01-AUG-1998 (TREMBLREL. 07
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148AA LONG HYPOTHETICAL P
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                                                 DNA RES. 4:141-150(1997).

DNA RES. 4:141-150(1997).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILAK EMBL; AB002325; D1021623; -.

EMBL; AB002325; CADHERIN; 5.

PROSITE; PS00232; CADHERIN; 5.

PFAM; PF00028; CADHERIN; 6.

CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; SEQUENCE 820 AA; 89864 MW; 3B6ECA92 CRC32;
                                                                                                                                                                                                                                                                                                                                                                      NAGASE T., ISHKAWA K., NAKAJIMA D., OHIRA M., SEKI
TANAKA A., KOTANI H., NOMURA N., OHARA O.;
"Prediction of the coding sequences of unidentified
The complete sequences of 100 new cDNA clones from k
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DNA RES. 5:55-76(1998)
EMBL; AP000005; D10312
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KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y., SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y., SAKAI M., OGURA K., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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ARCHAEA; EURYARCHAEOTA;
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EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
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nes 6; Conser
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01-JUN-1998
01-AUG-1998
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049927
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

CASTILLO J., MARQUEZ J.A., FRANCO L., BALLESTAR E., F
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; Y11207; E321874; -
SEQUENCE 483 AA; 54662 MW; D4481891 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PISOM SATIVUM (GARDEN PEA).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERWATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
FABALES; FABACEAE; PAPILIONOIDEAE; PISUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA EMBL; U7530; G1911278; -. PFAM; PFOM317; ribonucleo_red; 1. SEQUENCE 593 AA; 65952 MW; OB19B9ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBONUCLEOTIDE REDUCTASE LARGE SUBUNIT.
ORGYIA PSEUDOTSUGATA NUCLEAR POLYHEDROSIS VIRUS.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TREMBLREL.
01-JUL-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of the Orgyia polyhedrosis virus genome."; VIROLOGY 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. ROHRMANN G.F.;
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G (TREMBLREL.
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llarity 58.3%;
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04, LAST SEQUENCE UPDATE)
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Pred.
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No.
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3.79e+00;
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2.36e+00;
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RESULT 15
10 069782,
AC 069782,
DT 01-AUG-1998 (TREMELREL. 07, CREATED)
DT 01-AUG-1998 (TREMELREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMELREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMELREL. 07, LAST ANNOTATION UPDATE)
DT 0APA.
GN DAPA.
CS SINORHIZOBIUM MELILOTI.
OG PLASMID PRMEGR4B.
OC BACTERTA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACE DATA BACTOR RIZOBIACEAE; SINORHIZOBIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GR4;
RA SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SEQUENCE SINORHIZOBIOTO; -.
KW PLASMID.
SQ SEQUENCE 300 AA; 32297 MW; 7992E15D CRC32;
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Search completed: Fri Jun 11 17:31:55 1999 Job time: 127 secs.
                                                                                                                                                                                                                  Ouery Match 51.9%; Score 56; DB 2; Length 300; Best Local Similarity 50.0%; Pred. No. 6.05e+00; Matches 7; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-GR4;
ZEKRI S., GARCIA-RODRIGUEZ F., TORO N.;
ZEMNITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ222715; E1286070; -.

PLASMID.
SEQUENCE 300 AA; 32297 MW; 7992E15D CRC32;
                                                                                                       260 AAMKLLGRPGGEIR 273
::| ||:| ||:|
1 TPMFLLSRNTGEVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SINORHIZOBIUM MELILOTI.
ALASMID PRWEGR4B.
ALTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
HIZOBIACEAE; SINORHIZOBIUM.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:43:07 1999; MasPar time 4.85 Seconds 65.749 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-5
Description: (1-15) from US08991628.pep
Perfect Score: 113

1 CECNIKVKDVNDNFP 15

Scoring table: PAM 150 Gap 15 Sequence:

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part34

Statistics: Mean 18.398; Variance 59.622; scale 0.309

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1 2 3 5 5	Score 113 113 102 89 72 57		たっち9487000	DB 20 19 21 21 21 21 21 21 21 21 21 21 21 21 21	WIND WOLL	115845 97445 115869
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w	102	90.3	614	19	W07908	
4	89	78.8	778	21	W15489	
տ	72	63.7	787	17	R86865	
0	57	50.4	780	24	W25634	
7	57	50.4	780	21	W13130	
80	56	49.6	83	39	W84311	
9	56	49.6	1822	10	R55273	
10	54	47.8	43	11	R58865	
11	54	47.8	43	17	R87107	
12	53	46.9	83	29	W55470	
13	53	46.9	87	29	W55280	
14	52	46.0	11	21	W13139	
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Drosophila FRU 2 poly		gment	ċ	1 fragment (domai	5-Pfs28C f	Tbv25-Pfs28B fusion p	ragment	Segment of desmosomal	25 kD surface antigen	Human secreted protei	Plasmodium falciparum	WD-40 domain-contg. C	Stimulator of iron tr	Streptococcus pneumon	9	Rat full length cadhe	Human cadherin-8.	Full length human cad	Truncated rat cadheri	Rat truncated cadheri	Protocadherin clone R		Sequence encoded by O	Homo sapiens protocad	Phospholipase D.	Variant beta-lactoglo	Wild type beta-lactog	Ethyl esterified bovi
3.05e+02	0.0		3.05e+02			÷	•	•	•		2.44e+02			2.44e+02				in	i	in	in	in	i.n	i.	1.56e+02	'n	in	i,

ALIGNMENTS

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disease and which binds to the polypeptide to activate autoreactive T-cells in individuals with the autoimmune disease. This peptide is derived from the human desmoglein 3 protein (amino acids 251-265) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein protein are described in W04841-47. Sequence 15 AA;	tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II protein, such as HLA-DR, which is associated with a human autoimmune	<pre>8pp; Engl arations human nor hich is o isolated</pre>	wPI; 96-425218/42. Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for aldentification of other self and non-self antigens implicated in anti-impure disease.	Homo sapiens. W09627387-Al. 12-SEP-1996. 07-MAR-1996; U03182. 07-MAR-1995; US-400796. 07-MARD) HRAVVARD COLLEGE. (HARD) HRAVVARD COLLEGE. Strominger JL, Wucherpfennig KW;	W04845 standard; peptide; 15 AA. W04845; 18.FEB-1997 (first entry) 18.FEB-1997 of desmoglein 3, implicated in autoimmune disease. Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris; desmoglein; multiple sclerosis; herpes simplex virus; adenovirus; phosphomannomutase; human papillomavirus; Epstein-Barr virus; DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

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RESULT
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                    Fused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris Claim 1: Page 7-9: 9pp; Japanese.

W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients wit pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgG1 hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure, Fig 7: 50pp; English.

This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a ceil adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-1997 (first entry)
Pemphigus vulgaris antigen protein extracellular region.
Pemphigus vulgaris antigen protein extracellular region.
Putoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
Putoantibody; pemphigus vulgaris; PV; bulla; blister; skin disease;
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WPI; 93-00
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J08188540-A.
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27-NOV-1991; 798918.
27-NOV-1991; US-798918.
(USSH) US DEFT HEALTH 6.
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R30742 standard;
                                                                                                                                                                                         pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatology.
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                                                                                                                                               the resulting fusion phigus vulgaris. uence 614 AA;
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igus vulgaris; skin disease; autoantibodies;
       Similarity
14; Conser
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Similarity 100.0%;
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   90.3%;
larity 93.3%;
Conservative
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V, Stanley JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      614 AA.
Score 102; DB 19;
Pred. No. 6.20e-04;
0; Mismatches 1
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Pred. No. 3.
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3.31e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pemphigus foliaceus antigen-IgG constant region fusion protein - linked through the hinge region used to treat pemphigus foliaceus Claim I; Page 10:12; 17pp; Japanese.

This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus is antigen protein through the hinge portion. Pemphigus foliaceus is antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion protein is immunobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful immunodiagnosis. The fusion protein has little or no side effects.
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Best Local :
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12-SEP-1995; 260899.
12-SEP-1995; JP-2608
(NISH/) NISHIKAWA T.
WPI; 97-241758/22.
P-PSDB; T66428.
Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities Claim 15; Page 115-119; 146pp; English.

R86865-R86867 represent the sequences for three protocadherins. Th sequence represents the human protocadherin pc3. These sequences a related to cadherin, and possess cell adhesive ability. Cadherins glycosylated integral membrane proteins that are involved in cell-c
                                                                                                                                                             04-JAN-1996.
26-JUN-1995; U08071.
27-JUN-1994; US-268161
                                                                                                                                                                                                                                                                                                                   R86865
                                                                                                                Suzuki S;
WPI; 96-068873/07.
                                                                                                                                                                                                          Homo sapiens. WO9600289-A1.
                                                                                                        N-PSDB; T03572.
                                                                                                                                    (DOHE-) DOHENY EYE
Suzuki S;
                                                                                                                                                                                                                                         catenin; therapy.
                                                                                                                                                                                                                                                       Protocadherin; pc3;
                                                                                                                                                                                                                                                                     Human protocadherin
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27-AUG-1996
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Sequence 778 AA;
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nes 12; Conser
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80.0%;
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Pred. No. 1.85e-02;
2; Mismatches 1;
                                                                                                                                                                                                                                                         human;
                                                                                                                                                                                                                                                         rat;
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adhesion. Cadherins are composed of an N-terminal extracellular domain which consists of 5 unique subdomains, a membrane spanning domain, and

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                                                                                                                                                                               FIT Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion
PS Claim 1; Column 69-72; 56pp; English.

CC This sequence represents human cadherin-5. The invention specifically
CC provides details of human cadherin-5, -8, -11, -12 and -13, and rat
CC cadherin-8, -5, -11 and -13. Cadherin are calcium-dependent cell
CC adhesion proteins. They are glycosylated integral membrane proteins
CC that have an N-terminal extracellular domain that determines binding
CC specificity, a hydrophobic membrane spanning region and a C-terminal
CC sytoplasmic domain, which is highly conserved among members of the
CC through eatenins and other cytoskeleton-associated proteins. The
CC convel cadherin proteins may be used in the analysis of the role of
CC cadherins in various cancers. Sequence analysis of the cadherin
CC cadherin also allows investigation of the structure and function of
CC cadherin. The cadherin proteins may be isolated by using anti-cadherin
CC anthodies. These antibodies may also be used to modulate the activity
CC featherin and to determine the tissue specific distribution of cadherin
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Best Local
                                                                                 Query Match
Best Local Similarity
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1997.
17-APR-1992;
19-APR-1993;
19-APR-1993;
17-APR-1992;
01-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal cytoplasmic domain. The cytoplasmic domain interacts with the cytoplasmic domain is and other cytoskeleton associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These sequences were isolated using primers 1 and 2 (see T03575 and T03576) The proteins may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of these protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protocadherins, an secuence 787 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T85401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5646250-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cadherin; rat; calcium-dependent cell adhesion protein;
superfamily; cytoskeleton; eatenin; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cadherin-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W25634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W25634 standard;
                                                                                                                                                                    proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DOHE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 csvsvkvldvndnfp 345
                               135 ikvhdvndnwp 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOHENY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                    Each subclass
                                                                                                                                      780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 872643.
; US-049460.
; US-872643.
; US-332638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.7%;
                                                                                 50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                      of cadherins has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
2; M
                                                                   Score
Pred.
0; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     omains, a membrane spanning domain, and a The cytoplasmic domain interacts with the
                                                                 re 57; DB 24; I
d. No. 4.98e+01;
Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
1.36e+00;
                                                                                                                                                                  unique tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 787
                                                                                                   Length 780
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Best Local
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19-APR-1993; 1
26-JAN-1994; 1
                                                                                                                                                                                                                                                                   18-DEC-1998.
05-MAR-1998;
31-MAR-1997;
                                        Disclosure; Page 16-17; 24pp; Japanese.

The present sequence is used to demonstrate the method of the invention. The specification describes the comparison of DNA base sequences. The method involves 3 steps of: (1) division of a first and second nucleic acid sequence into base groups of three base lengths, and translation into amino acids; (2) all base and amino acid insertions and deletions of the two nucleic acid sequences are observed and the amino acid sequences encoded by these nucleic acid sequences are compared; and (3) adjacent bases and amino acids are compared and step (1) repeated after shifting the translation frame by one base towards the 3' end or shifting the translation frame one base towards the 3' end, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on homologous rat cacherin cDNA.

Antibodies or fragments that specifically bind the human can be used to purify the cacherin, determine its tissue and antagonise its ligand/antiligand binding activities.

Sequence 780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W13130 standard;
W13130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Full length huma
Ca2+ dependent;
                                                                                                                                                                                                        WPI; 99-110965/10.
Comparison of DNA base sequences -
insertions and deletions
                                                                                                                                                                                                                                       WPI; 99-110965/10.
                                                                                                                                                                                                                                                                                                                               Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Columns 75-78; 59pp; English.
The present sequence is full length human cadherin-5, which
is a Ca2+ dependent cell adhesion protein. The human cadherin
was isolated from a placental cDNA library, using probes based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 97-108328/10.
N-PSDB; T61921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain;
                                                                                                                                                                                                                                                                                                                                             DNA sequence
                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                           W84311;
18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                       T 8
W84311 standard; Protein; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies to cadherin proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue expression;
             encompassing four bases, and not translating the second or third base. The new method {\bf 1}_{\bf 2} useful for comparing DNA base sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DOHE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 ikvhdvndnwp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÇI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKVKDVNDNFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ependent; cell adhesion protein; placental; cadherin;
human; antibody; purification; determination;
expression; binding antagonist; calcium ion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 81.8% 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOHENY EYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
human cadherin-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-872643.
US-049460.
US-188228.
                                                                                                                                                                                                                                                                    053102.
JP-079586.
                                                                                                                                                                                                                                                                                                                                             comparison
                                                                                                                                                                                                                                                                                                                                                             sequence used
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 21; Le
Pred. No. 4.98e+01;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                              exemplify the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful
                                                                                                                                                                                                                          using accurate observations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cadherin antagonists,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes based
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                                                                                                                                                                                                                                                                                                                                                                                           pri plagnosing presence of abnormal epithelial tissue in vitro - utilises monoclonal antibodies to alpha6 beta4 cell surface protein Example 5; Figure 9; 34pp; English.

Example 5; Figure 9; 34pp; English.

Integrins are heterodimers comrised of alpha and beta subunits, that are non-covalently associated transmembrane glycoproteins. Il alpha chains and 6 beta chains have been recognised in man. Each alpha subunit tends to associate with only one type of beta subunit but there are several exceptions. Integrins mediate (in part) the interaction of cells with the extracellular matrix, forming a link between the extracellular matrix and the cytoskeleton. They may transmit signals from the extracellular to the intracellular environment, affecting cell behaviour. This sequence is the beta4 subunit of an alpha6 beta4 integrin.
                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches
R58865 standard; Protein; 43 AA. R58865; 17-ARR-1995 (first entry) Rat-224 cadherin partial sequence. Cadherin; cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-1987; US-016552
04-JAN-1989; US-293384
01-OCT-1990; US-591105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta subunit of integrin cell surface receptor. Integrin; alpha; beta; subunit; glycoprotein; heterodimer; transmembrane; extracellular matrix; cell signalling; cytoskeleton; behaviour; signal transduction; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R55273;
31-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R55273 standard; Protein; 1822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kajiji S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KAJI/) KAJIJI S.
(QUAR/) QUARANTA V.
                                                                                                                                                                                                650 ecnfkvkmvde 660
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2 ECNIKVKDVND 12
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19-FEB-1987;
                                                                                                                                                                                                                                                                                    49.6%;
Local Similarity 63.6%;
nes 7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 40.0%; hes 6; Conservative
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617
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Pred.
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Mismatches 5;
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6.28e+01;
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                                                                                                                                                                                                                                                                                                                                             Length 1822;
                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC C-terminus of the fourth extracellular subdomain (EC-4) were CC identified. The corresp degenerate oligos (068949, 068950) were CC designed for use as PCR primers PCR was carried out on a rat brain CC DNA prepn. Two major bands of about 450 bps and 130 bps were found. The 450 bp band corresponded to the expected length between the two CC primer sites, but the 130 bp band could not be predicted from any CC of the previously identified cadherin sequences. The 450 bp and 130 cC of the previously identified cadherin sequences. The 450 bp and 130 cC clones were extracted and sequenced. Nineteen novel partial cDNA CC clones (including sequences corresp. to the PCR primers) are given in Q68951-Q68969 and R58860-R58878. The deduced AA sequences of the CC cDNA clones are homologous to, but distinct from the known cadherins. The cadherins described thus far have highly conserved CC chas sequences in the EC-3 including the consensus sequence CC corresp. sequences in R58879 or R58880 at its end, while the CC corresp. sequences of other subdomains, except for the 5th extra-cc cellular subdomain (EC-5), are D-R-E and the sequence in R58881 creatively. In contrast the deduced AA sequences of the new CC clones that corresp. to cadherin extracellular subdomains include the sequence D-Y-E or D-F-E at one end, but have the sequence CC D-X-N-D-N-X-P-X-F instead of R58879 or R58880 at the other end. CC previously identified cadherins but did not show significant the converse of the sequences of the sequences of the partial clones are homologous to converse and converse of the sequence of converse and converse of the sequence of the sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 1
Polynucleotide(s) encoding human protocadherins pc3 epc5 - involved in cell-cell adhesion and regulation a Example 1; Page 40; 146pp; English.
R87102-R87120 represent partial fragments of the rat sequence. The cDNAs encoding these sequences were is
                                                                                                                                                                                                                                                                                                                                                                                            R87107
R87107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; Q68957.

Polynuclectide sequences encoding new proto:cadherins - useful for modulating natural binding and regulating activities.

Example; Page 38; 114pp; English.

Two regions of conserved AA sequence, one from the middle of the third cadherin extracellular subdomain (EC-3) and the other from the third cadherin extracellular subdomain (EC-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1994.
23-DEC-1993; U12588.
29-DEC-1992; US-998003
(DOHE-) DOHENY EYE INST
                                                                                                           WPI; 96-068873/07.
N-PSDB; T03582.
                                                                                                                                                                                                                                                                                                    Protocadherin clone RAT-224. Protocadherin; pc3; pc4; pc5; catenin; therapy; clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNAs appear molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 94-293849/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus rattus.
WO9414960-A.
                                                                                                                                                     Suzuki S;
                                                                                                                                                                                                26-JUN-1995;
27-JUN-1994;
                                                                                                                                                                                                                                          04-JAN-1996.
                                                                                                                                                                                                                                                            Rattus rattus.
WO9600289-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                         (DOHE-)
                                                                                                                                                                                                                                                                                                                                                                     28-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CECNIKVKDVNDNFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ckiiikvvdvndnap 43
                                                                                                                                                                                                                                                                                                                                                                                                                standard; Peptide; 43
                                                                                                                                                                            DOHENY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                U08071.
US-268161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprise a new subclass of cadherin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.88;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 11; Le
Pred. No. 9.93e+01;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                           human; rat; cadherin; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 43
      it protocadherin isolated after
                                                                and pc4 and activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                       rat
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88888888888888888

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Helicobacter pylori nucleic acid sequences and encoded prolypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection for diagnosis of H. pylori infection for treat H. pylori claims 14,94; page 677-678; 1145pp; English.

CC This sequence is a H. pylori secreted protein.

CC The protein may be used in a vaccine to prevent or treat H. pylori claims in the protein may be used in a vaccine to prevent or inhibitors. The cuseful as potential H. pylori life cycle activators or inhibitors. The CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic cacid sequences complementary to the DNA act as antisense sequences and cc and sequences complementary to the DNA act as antisense sequences and captive the protein can be used in immunoassays to evaluate the abundance against the protein can be used in immunoassays to evaluate the abundance of the pylori (ATCC 55679) was determined from overlapping contic sequence of the pylori specific antigens. The genomic sequence of the pylori (ATCC 55679) was determined from overlapping contics generated by mechanically shearing the bacterial DNA. The sequences were analysed for vaccine development, the amino acid sequences predicted coding regions cc defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported conterest, particular regions can be isolated from H. pylori by PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc screening a rat brain cDNA preparation with the primers shown in T03575 cc and T03576. The primers were constructed from portions of the amino acid c sequences of the third and fourth extracellular domains of published cc cadherin sequences. The full length cDNA sequence encoding rat crowdherin pc5 is represented in T03574. The cytoplasmic domain of cadherin interacts with the cytoskeleton through catenins and other cytoskeleton associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These protein sequences are involved in cell-cell adhesion. These sequences may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of these protocadherins, and can be used therapeutically.
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Best Local
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27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WB54/0;
24-UNN 1998 (first entry)
H. pylori ORF 06apil119_16594193_fl_9 secreted protein.
Cytoplasmic; vaccine; prevention; treatment; infection;
identification; binding compound; bacteria; life cycle;
identification; duodenal ulcer disease; chronic gastritis; d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori. W09737044-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W55470 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V24879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 ckilikvvdvndnap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                  particular regions can be isolated from H. pylori by ion for recombinant polypeptide production, e.g. in F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%;
larity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54; DB 17; Le Pred. No. 9.93e+01; 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  envelope;
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RESULT
ID WI
AC WI
DT 14
DE HI
KW CC
KW PI

JT 14 W13139 standard; Protein; W13139;

A

14-MAY-1997 (first entry)
Human cadherin-Lantigenic epitope (residues 242-252).
Ca2+ dependent; cell adhesion protein; cadherin; human; antibody; purification; determination; epitope; tissue expression; binding antagonist; calcium ion; antigen.

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1 CECNIKVKDV 10

Matches

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2

Indels

0;

Gaps

0

Similarity

47 cncnikipsi 56

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                                                                                                        Pri Helicobacter pylori nucleic acid sequences and encoded pri Helicobacter pylori nucleic acid sequences to treat or prevent H. pylori prolipheride(s) - useful in vaccines to treat or prevent H. pylori finfection and for diagnosis of H. pylori infection Pri finfection and for diagnosis of H. pylori infection Pri finfection and for diagnosis of H. pylori protein of unspecified function. Prince the protein may be used in a vaccine to prevent or treat H. pylori C. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, in the protein as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of C. H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and C. can be used to prevent the translation of H. pylori mRNA. Antibodies and distribution of H. pylori-specific antigens. The genomic sequence of C. H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF certains. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR camplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches
                     Query Match
Best Local
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27-MAR-1997; U05223.
27-MAR-1996; US-761318.
06-DEC-1996; US-625811.
29-MAR-1996; US-758731.
22-APR-1996; US-758735.
25-OCT-1996; US-738905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic; vaccine; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W55280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori.
WO9737044-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; V24689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALM RA, SMITH D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; identification; dudenal ulcer disease; chronic gastritis; diagnosis.
                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            )2-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 cncnikipsi 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1:||||: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ა</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 (first entry)
ORF 11ge10309orf7 protein.
                                                                              87
 46.9%;
llarity 50.0%;
Conservative
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                                                                              AA;
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Score 53; DB 29;
Pred. No. 1.25e+02;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 29;
Pred. No. 1.25e+02;
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                                         Length 87
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(DOHE-) DOHENY EYE INST. Suzuki, 97-108328/10. Antibodies to cadherin proteins - useful as cadherin antagonists,

Homo sapiens. US5597725-A. 28-JAN-1997. 17-APR-1992; 872643. 17-APR-1992; US-872643. 19-APR-1993; US-049460. 26-JAN-1994; US-188228.

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                                                                                                                                                                                                    Detection of t(1,19) break-point-associated genes E2A and pr1 -
pri Detection of t(1,19) break-point-associated genes E2A and pr1 -
pri chromosomal translocation, and prods. useful in diagnosis and
prods. useful in diagnosis and
prods. useful in diagnosis and
prods. useful in diagnosis and
prods. useful in diagnosis and
prods. The E2A gene (see Q13669), encoding immunoglobulin enhancer-binding
factors E12 and E47 (see Q13670 and Q13671), is localised to the
production of a consistently recurring chromosomal translocation
present in many acute leukemias and is structurally altered by most
t(1,19) chromosomal translocations. The translocation results in
present in many acute leukemias and is structurally altered by most
t(1,19) chromosomal translocations. The translocation results in
present in many acute leukemias and is structurally altered by most
th(1,19) chromosomal translocations. The translocation results in
present in many acute leukemias and is structurally altered by most
th(1,19) chromosomal translocations. The translocation results in
the translocation many (see Q13672 for fusion cDNA) that crosses
the breakpoint between chromosome 1 and 19.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
The cDNAs of E12 and E47 encode nearly identical proteins conty.
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Matches
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02-FEB-1991; U01168.
23-FEB-1990; US-484063.
23-FEB-1990; US-484063.
(STRD ) LELAND STANFORD JR UNIV.
(WHIT-) WHITEHEAD INST BIOMED RE.
CLEARY ML, Mellentin JD, Baltimore D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E47 cDNA prod. (pE47P).
Immunoglobulin; enhancer-binding factor; E12; E47; E2A;
chromosomal translocation; leukemia; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             л 15
R13947 standard; Protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q13671.
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                                                  82 vrvrdineaf 91
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IKVKDVNDNF 14
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                                                                                                        Similarity
4; Conser
                                                                                                     46.0%;
larity 40.0%;
Conservative
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                                                                                                     Score 52; DB 3; L
Pred. No. 1.56e+02;
5; Mismatches 1
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                                                                                                                                                  Length 132
                                                                                                     1; Indels
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                                                                                                     0;
                                                                                                     Gaps
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Qy Dy

1 vtlqdindnfp 11 : : |:|||| 5 IKVKDVNDNFP 15 Query Match

Best Local Similarity 54.5%;

Matches 6; Conservative

Score 52; DB 21; Pred. No. 1.56e+02; 3; Mismatches 2

Length 11; 2; Indels

0;

Gaps

0

Claim 5; Column 112; 59pp; English.

The present sequence is an antigenic epitope from human cadherin-5, which is a Ca2+ dependent cell adhesion protein. Antibodies or fragments that specifically bind the epitope can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 11 AA;

Search completed: Fri Jun 11 17:44:58 1999 Job time: 111 secs.

<u></u> _
,
(ME)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Fri Jun 11 17:38:59 1999; MasPar time 4.29 Seconds 140.011 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-991-628-5 (1-15) from US08991628.pep 113 1 CECNIKVKDVNDNFP 15

Scoring table:

PAM 150 Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 25.852; Variance 36.674; scale 0.705

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

Query Match Best Local Si Matches 15	#journal Cell (1 #1title #1title pemph) #cross-references MUII #cross-references MUII #accession A41088 ##molecule_type mRR ##molecule_type mRR ##residues 1.5 ##cross-references GDB:DSG: ##gene ##cross-references femap_position 18912.1. CLASSIFICATION #superfc calcium trans; FEATURE 1-23 #dd 24-49 #p. 50-999 #p. 50-615 #dd 24-49 #p. 50-267 #dd 390-495 #dd 496-598 #dd 496-598 #dd 496-598 #dd 496-999 #dd 490-938	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors
h 100.0%; Score 113; DB 1; Length 999; Similarity 100.0%; Pred. No. 3.28e-12; 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Cell (1991) 67:869-877 Autoantibodies against a novel epithel pemphigus vulgaris, a disease of cel pemphigus vulgaris, pipe status perdain vulgaris, cadherin repeat status predicted percoduct desmoglein homology status vulgaris, a domain cadherin repeat homology widomain desmoglein repeat wilabel widomain desmoglein repeat wilabel wilab	IJHUG3 #type complete desmoglein 3 precursor - human pemphigus vulgaris antigen #formal_name Homo sapiens #common_name man #formal_name Homo sapiens #comm

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##cross-references GB:S64268; GB:S64270
A37785
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##note this sequence has been revised in references A38872 and
S38721
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Complete sequence of the desmoglein precursor and evidence for the existence of different desmoglein genes expressed in cell type-specific patterns.
                                                                                                                                                                                                                                                        Koch, P.J.; Walsh, M.J.; Schmelz, M.; Goldschmidt, M.D.; Zimbelmann, R.; Franke, W.W.
Eur. J. Cell Biol. (1990) 53:1-12
Identification of desmoglein, a constitutive desmosomal glycoprotein, as a member of the cadherin family of cell adhesion molecules.
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Similarity 80.0%;
12; Conservative
                                                                                                                                      Wagner, R.M.; Green, K.J.
J. Cell Sci. (1991) 99:809-821
Structural analysis and expression of human
cadherin-like component of the desmosome.
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desmosomal glycoprotein I
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
26-Feb-1998
Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Rees, D.A.; King, I.A.; Magee, A.I. Biochem. Soc. Trans. (1991) 19:1060-1064 . Desmosomal glycoproteins I; II and III: no
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                                                                                                                                                                                                                                                                                                                                    Desmosomal glycoprotein DGI, a compor desmosome junctions, is related to cell adhesion molecules.
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FEATURE
5-45
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#mag_position 18q12.1-18q12.2
CLASSIFICATION #superfamily cadherin; cadherin
KEYWORDS calcium hinding.
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DATE
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50-1049
50-548
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#cross-references MUID:92175187
#accession A61279
                                                                                                                                                                                                                                                                                                                              #submission #accession
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                                                                                                                                                                                                                                              ##molecule_type DNA
##residues 1-171 ##label MCL
##cross-references EMBL:Z67999; NID:g1067216; PID:g1067219
                                                                                                                                                                                                                                                                                                             ##status
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##residues 1-55 ##label WH3
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                                                                                        Local
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                                     CQCSVKIRSVLTDF 89
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   CECNIKVKDVNDNF
                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                            McLean, J.; Harris, D. submitted to the EMBL Data Library, S62588
                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SPAC21E11.03c - fission yeast (Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
16-May-1996 #sequence_revision 13-Mar-1997 #text_change
31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
                                                                                                                                             #domain
#length 171
                                                                                                                                                                                               #superfamily fos/jun DNA-binding domain homology
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                                                                     58.4%;
larity 35.7%;
Conservative
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#binding_site carbohydrate (
    predicted
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#domain desmoglein repeat #label DG2\
#domain desmoglein repeat #label DG3\
#domain desmoglein repeat #label DG3\
#domain desmoglein repeat #label DG4\
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#domain propeptide *status predicted *label PRO\
#product desmoglein *status predicted *label MAT\
#domain extracellular *status predicted *label EXT\
#domain cadherin repeat homology *label CR1\
#domain cadherin repeat homology *label CR2\
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Pred. No. 1.
2; Mismatc
                                                                       Score 66; DB 2; I
Pred. No. 9.35e-02;
6; Mismatches 3
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1.28e-06;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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135-189
203-258
272-324
336-389
                                                                                                                                    #journal
#title
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                                                                                              #cross-references MUID:92108053
                                                                                                                                                                                          #authors
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##residues 1-394 ##label BUL
##cross-references GB:U67560; GB:L77117; NID:g1591813; PID:g1591821;
##cross-references GB:MJ1193; PID:g1511192
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##molecule_type_mRNA
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                                                                                                                                                                                                                                                                 IJBODD #type fragment desmocollin 2b precursor - bovine (fragment) epithelial type 2 desmocollin subform II #formal_name Bos primigenius taurus #common_name cattle #formal_name #formal_name fragment formal_name fragment formal_name fragment formal_name fragment formal_name fragment formal_name fragment formal_name fragment formal.
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                                                                                                                                  Complexity and expression
                                                                                                                                                      Proc.
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#formal_name Methanococcus jannaschii
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R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.
R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty,
Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, F
                                                                                                                                                                                                                                                 05-Sep-1997
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ferredoxin 2[4Fe-4S] homology #label
ferredoxin 2[4Fe-4S] homology #label
ferredoxin 2[4Fe-4S] homology #label
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ferredoxin 2[4Fe-4S] homology #label
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Pred. No.
3; Misma
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No. 3.57e-01
                                                                                                                                    patterns
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FEATURE 1-89

90-809 90-645 92-197

GENETICS

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#gene
CLASSIFICATION
KEYWORDS
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312-423
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673-863
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312-423
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527-634
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##experimental_source muzzle
##note sequence extracted from NCBI backbone
##note 264-Gln and 333-Gln were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues
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Local Similarity 61.5%;
hes 8; Conservative
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epithelial type 2 desmocollin subform I
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
05-Sep-1997
                                                                                                                                                                                                                                                                                                                               #superfamily cadherin; cadherin repeat homology
alternative splicing; calcium binding; cell adhesion;
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alternative splicing; calcium binding; cell adhesion;
duplication; glycoprotein; transmembrane protein
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R.; Franke, W.W.
                                                                                                                                                                                                                                                                                                                duplication; glycoprotein; phosphoprotein; transmembrane
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                                                                                               #domain propeptide #status predicted #label PRO\
#product desmocollin 2a #status predicted #label MA'
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR3\
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#product desmocollin 2b #status predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR3\
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#domain cadherin repeat homology #label CR5\
                       #binding_site carbohydrate (Asn)
predicted\
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binding_site phosphate (Ser) (covalent) #status
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Pred. No. 1.31e+00;
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275 ECPIATKTINEEYP 288
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RESULT ENTRY

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Ş 밁 SUMMARY

646-672

Matches

FEATURE 1-89

90-863 90-645 92-197

GENETICS

KEYWORDS

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Query Match 53.1%;
Best Local Similarity 69.2%;
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Best Local Similarity 61.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:95403557
                                                                                                                                      ##status preliminary
##molecule_type DNA
##molecules 1-527 ##label BAD
##cross-references EMBL:Z56276; NID:g1022345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
##residues 1-896 ##label YUE
##cross-references GB:L33774; NID:g914820;
Similarity 42.98 6; Conservative
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T.; Chidgey, M.A.; Garrod, D.R.
J. Cell Sci. (1995) 108:2163-2173.
Characterisation of a desmocollin isoform (bovine DSC3)
extensively expressed in lower layers of stratified
                                                                                                                                                                                                                                                                                                                  S62484 #type complete
hypothetical protein SPAC468.07c - fission
(Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
16-May-1996 #sequence_revision 13-Mar-1997
                                                                   125/1; 158/2; #length 527 #
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19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change
13-Mar-1998
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1 863 #checksum 1299
                51.3%;
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the EMBL I
                                                                     #molecular-weight 59613 #checksum
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Pred. No. 1.31e+00;
1; Mismatches 3
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Pred. No. 1.31e+00;
3; Mismatches 2
              Score 58; DB 2; 1
Pred. No. 3.06e+00;
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 Mismatches
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Best Local Similarity 42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                     #authors Saka, Y.; Sutani, T.; Yamashita, Y.; Saitoh, S.; Takeuchi,
M.; Nakaseko, Y.; Yanagida, M.
#journal EMBO J. (1994) 13:4938-4952
#title Fission yeast cut3 and cut14, members of a ubiquitous protein family, are required for chromosome condensation and segregation in mitosis.

#cross-references_MUID:95045386
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##restidues 1-832 ##label BOE
##cooss-references EMBL:X83228; NID:g854174; PID:g854175
#ETCATION #superfamily cadherin repeat homology
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##cross-references EMBL:D30788; NID:g577659; PID:d1007025; PID:g603501
#Y #length 1324 #molecular-weight 150593 #checksum 3330
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Local Similarity 64.3%;
nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S51622 #type complete
cut3 protein - fission yeast (Schizosaccharomyces pombe
#formal_name Schizosaccharomyces pombe
15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
09-Sep-1997
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15-Jul-1995 #sequence_revision 01-Sep-1995
10-Sep-1997
DNA replication protein DnaC - #formal_name Aquifex aeolicus 08-May-1998 #sequence_revision
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     08-May-1998 #text_change
                                      Aquifex aeolicus
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Best Local Similarity 63.6%;
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#title
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#journal Cell Regul. (1991) 2:261-270
#title Diversity of the cadherin family: decrease of the cadherin family: decrease multi-91283540
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##cross-references GB:AE000713; NID:g2983424;
##experimental_source strain VF5
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                  ##molecule_type protein

48-60,'X',62,'X',64;108-116,'X',118-123;237-238,'X',240,
##residues

'X',242-252,'X',254-256;263-275,'X',277-283,'X',285;

"X',242-252,'X',425-429 ##label LAM
##experimental_source cultured endothelial cells
##experimental_source cultured endothelial cells
                                                                                                                                                                                                                                                                                                     ##residues 5-516,'I',518-784 ##label SUZ ##cross-references EMBL:X59796; NID:g639976; PID:g29593
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!NCE $24305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breviario, F.; Caveda, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lampugnani, M.G.; Dejana, E. submitted to the EMBL Data Library, June 1994 Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a novel endothelial specific cadherin.
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A novel endothelial-specific membrane protein is a notell-cell contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cadherin 5 precursor - human 784 antigen; cadherin, endothelial-specific; VE-cadherin #formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S49893; S24305; A43418
S49893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-784 ##label
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sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #type complete
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Pred. No. 4.65e+00;
2; Mismatches 2
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Best Local Similarity 81.8%;
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                     Abu-Alfa, A.; Soleimani, M.; Aronson, P.S.
#journal J. Biol. Chem. (1995) 270:17594-17601
#title Isolation and cDNA cloning of Ksp-cadherin, a novel kidney-specific member of the cadherin multigene;
#cross-references MUID:95340560
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523,535
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                                                                                                                                                                                                                                                         ##residues 1-829 ##label THO
##cross-references EMBL:U28945; NID:g902885; PID:g902886
# #length 829 #molecular-weight 88827 #checksum
                                                                                                                                                                                                                                                                                                                                                   ##status
                                                                                                                                                                                                     Match 50.4%;
Local Similarity 53.3%;
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NCBIP:113051, NCBIP:113054)
Cadherins mediate calcium-dependent intercellular adhesion, and are thought to be involved in the sorting of different cell types
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calcium binding; cell adhesion; duplication; glycoprotein;
IJHUDB #type complete desmocollin 3b precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change
14-Feb-1997
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#formal_name
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#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR4\
#domain cadherin repeat homology #label CR4\
#domain cadherin repeat homology #label CR5\
#domain transmembrane #status predicted #lab
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1784 #molecular-weight 87516
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n - rabbit
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intracellular #status predicted #label INT\
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Pred. No. 4.65e+00;
2; Mismatches !
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Pred. No. 4.
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Search completed: Fri Jun Job time: 87 secs.

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ACCESSIONS
REFERENCE
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#map_position 18q12.1-18q12.1

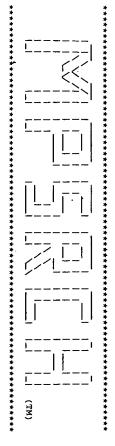
CLASSIFICATION #superfamily cadherin; cadherin repeat homology

alternative splicing; calcium binding; cell adhesion;

KEYWORDS duplication; glycoprotein; phosphoprotein; transmembrane
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GENETICS
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Best Local
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#title Desmosomal glycoproteins II and III. Cadherin-
molecules generated by alternative splicing.
#cross-references MUID:91244819
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136-695
                                         341 CIINIDDVNDHLP 353
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##note it is uncertain whether Met-1 is the initiator

whether translation is initiated upstream to
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##residues 1-847 ##label PAR
  ω
  CNIKVKDVNDNFP
                                                                               h 50.4%;
Similarity 53.8%;
7; Conservative
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K.J.; King, I.A.; Koch, P.J.; Magee, A.
Stanley, J.R.; Steinberg, M.S.
J. Cell Biol. (1993) 121:481-483
Nomenclature of the desmosomal cadherins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation; nomenclature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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#domain intracellular *status predicted *label INT\
#binding_site carbohydrate (Asn) (covalent) *status
predicted
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#domain propeptide #status predicted #label PRO\
#product desmocollin 3b #status predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR4\
#domain cadherin repeat homology #label CR5\
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Pred. No. '
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OMIM:600271
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A.I.; Rees,
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:36:11 1999; MasPar time 2.45 Seconds 172.800 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: >US-08-991-628-5 (1-15) from US08991628.pep 113

Sequence: 1 CECNIKVKDVNDNFP 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 l:swissprot

Statistics: Mean 26.658; Variance 31.710; scale 0.841

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20

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DSG3_HUMAN DSG1_BOVIN DSG1_BOVIN DSG1_SCHPO DSC2_BOVIN SYR_CAEEL OBP_HSV62 OBP_HSV62 OBP_HSV60 DSC2_MOUSE YAD7_SCHPO CCUT3_SCHPO CCUT3_SCHPO CCUT3_SCHPO CCUT3_SCHPO CTUT3_SCHPO CTUT3_SCH	Ħ
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6.78e-15 2.56e-08 1.22e-02 2.61e-01 4.27e-01 4.27e-01 4.27e-01 4.27e-01 1.12e+00 1.1	Pred. No.

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HYPOTHETICAL PROTEIN T HYPOTHETICAL 375.7 KD	DNA POLYMERASE (EC 2.7	VACUOLAR ASSEMBLY PROT	DNA REPLICATION LICENS	PHOSPHOLIPASE D PRECUR	DNA REPLICATION LICENS	TRANSLATION INITIATION	HYPOTHETICAL 48.1 KD P	CANDIDAPEPSIN 6 PRECUR	CANDIDAPEPSIN 4 PRECUR	D-NOPALINE DEHYDROGENA	L-ASPARAGINASE I (EC 3	DNAJ-LIKE PROTEIN MG00	TRANSCRIPTION FACTOR E	PROBABLE METHIONINE AM	BETA-LACTOGLOBULIN PRE	BETA-LACTOGLOBULIN.	PHOSPHOLIPASE A2 PRECU	CONIDIAL GREEN PIGMENT	DNA POLYMERASE (EC 2.7	TRYPTOPHAN 5-MONOOXYGE
1.13e+01 1.13e+01	1.13e+0	1.13e+0	1.13e+01	1.13e+01	1.13e+01	7.21e+00	7.21e+00	7.21e+00												

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M76482; G190752; 41088; IJHUG3. 69615; E; PS00232; CADHERIN; 3. PF00028; cadherin; 4. P09803; 1EDH.	This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the EBLopean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).	- I- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS (POTENTIAL). - I- DISSASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISSASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. - I- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 92069753. MANAGAI M., KLAUS-KOVTUN V., STANLEY J.R.; "Autoantibodies against a novel epithelial cadherin in pemphigus "Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion."; CELL 67:869-877(1991). -i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. -i- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND	DSG3_HUMAN STANDARD; PRT; 999 AA. P32926; 01-OCT-1993 (REL. 27, CREATED) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 01-OVT-1997 (REL. 35, LAST ANNOTATION UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DESMOGLEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA). DSG3. HOMO SADIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

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BOS TAURUS (BOVINE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;

EUKARYOTA; METAZOA; CHORDATA; PECORA; BOVOIDEA; BOVIDAE.
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Q03763;
Q1-OCT-1993
Q1-OCT-1993
Q1-NOV-1997
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KOCH P.J.,
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DOMAIN
adhesion molecules.";
BIOCHEM. BIOPHYS. RES. COMMUN. 173:1224-1230(1990).
-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS FILAMENTS MEDIATING CELL-CELL ADHESION.
                                                                                                                                                                                  "Complete amino acid sequence of the polypeptide and identification of a seur. J. CELL BIOL. 55:200-208(1991).
                                                                                                                                                                                                                                                                                                                                                    glycoprotein, as a
molecules.";
                                                                                                                                                                                                                                                                                                                                                                   ZIMBELMANN R., FRANKE W.W.;
"Identification of desmoglein,
glycoprotein, as a member of t
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 44-1043 FROM N.A. TISSUE-MUZZLE EPITHELIUM;
MEDLINE; 91168965.
KOCH P.J., WALSH M.J., SCHMEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHWIDT M.D.,
SUBMITTED (MAR-1991) TO EMBL,
                                                                                         SEQUENCE OF 44-493 FROM N.A.
MEDLINE; 91097553.
GOODWIN L., HILL J.E., RAYNOR K., RASZI
"Desmoglein shows extensive homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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(REL. 35, LA
1 PRECURSOR
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                                                                                                                                                                                                                                                                                             OF.
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Pred. No. 6.78e-15;
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EMBL; X57784; G436062; -.
EMBL; M58165; G552318; -.
PIR; S14603; LUBOG1.
PROSITE; PS00232; CADHERIN;
                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
PRIMATES; CATARRHINI; HOMINID
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ARNEMANN J., RUTMAN A.J., BUXTON R.S., MAGEE A.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                 WHEELER G.N., PARKER A.E.,
                           TISSUE-KERATINOCYTES;
MEDLINE; 91271279-
                                              SEQUENCE FROM N.A.
                                                                                                      DESMOGLEIN 1
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1 CECNIKVKDVNDNFP
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TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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DESMOSOMAL S
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(REL. 27, L)
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1 PRECURSOR
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larity 80.0%;
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                                                                 HOMINIDAE;
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         PIDSLEY
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                                                                                                                                                                                                                                     Score 89; DB 1; pred. No. 2.56e-08
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PIR; S16906; IJHUG1.
MIN; 125670; -.
PROSITE; PS00232; CADHERIN; 2
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                                                                                                                  PCR1_SCHPO STANDARD; PRT; 171 AA.

009926;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR PCR1 (TRANSCRIPTION FACTOR PCR1 (TRANSCRIPTION FACTOR PCR1 OR MTS2 OR SPAC21E11.03C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
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REPEAT
                                                                  EUKARYOTA; FUNGI; ASCOMYCOTA; SCHIZOSACCHAROMYCETALES; SCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P09803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALCIUM-BINDING; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 CECNIKILDVNDNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CECNIKVKDVNDNFP 15
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FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIFILAMENTS MEDIATING CELL-CELL ADHESION.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND OESOPHAGUS.
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESMOSOMAL SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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180
1049
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llarity 80.0%;
Conservative
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N; SIGNAL;
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270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGI, a component of
the cadherin family
                                                               COTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 89; DB 1;
Pred. No. 2.56e-08
2; Mismatches
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DESMOGLEIN REPEAT 2
DESMOGLEIN REPEAT 2
DESMOGLEIN REPEAT 4
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POTENTIAL.
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                          MTS2).
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AND INTERMEDIATE
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RESULT
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Best Local Similarity
Matches 5; Conse
                                                                                                         01-FEB-1994
15-JUL-1998
DESMOCOLLIN
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity.";
activity.";
GENES DEV. 8:1693-1702(1994).
-I- FUNCTION: INVOLVED IN REGULATION
-I- FUNCTION BINDS AND ACTIVATES
                                                                                                                                                                                                DSC2_BOVIN
P33545;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEIOSIS.
DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Schizosaccharomyces pombe pcrl+ encodes a CREB/ATF protein involved in regulation of gene expression for sexual development."; MOL. CELL. BIOL. 16:704-711(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 96140438.
WATANABE Y., YAMAMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCLEAN J., HARRIS D., SUBMITTED (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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HSSP; P05412; 1FOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D63667; G1199496; -. EMBL; U87870; G1839252; -. EMBL; Z67999; E1168681; -. EMBL; Z67999; E1768681; -. PROSITE; PS00036; BZIP_BASIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (
or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95047325.
WAHLS W.P., SMITH G.R.;
"A heteromeric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (FEB-1997)
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                                             BOS TAURUS EUKARYOTA;
ARTIODACTYLA; RUMINANTIA;
                                                                                           DSC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            76 CQCSVKIRSVLTDF
                                                                                                                                                                                                                                                                                                                                     CECNIKVKDVNDNF
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             (BOYINE).
METĀŽOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
FR. DIMTNANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 AA;
                                                                                                                                  (REL.
(REL.
(REL.
2A/2B
                                                                                                                                                                                                                                                                                                                                                                                                                        58.4%;
larity 35.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
42
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                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                  28, CARATED)
28, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
PRECURSOR (EPITHELIAL TYPE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
66
19348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BARRELL B.G., RAJANDREAM M.A., TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVATOR; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 66; DB 1; Le
Pred. No. 1.22e-02;
6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASIC MOTIF.
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0D025155 CRC32;
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DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSION FOR RECOMBINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous
and hot spot
                                                                                                                                       DESMOCOLLIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WALSH
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HOT SPOT
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Best Local
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VARIANT
VARSPLIC
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CARBOHYD
CARBOHYD
DSC3_BOVIN STANDARD;
Q28060; Q28061; Q28176;
Q1-NOV-1997 (REL. 35, CR
                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complexity and expression patterns of the desmosomal cadherins.";
PROC. NATL. ACAD. SCI. U.S.A. 89:353-357(1992).

-: FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.

-! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-! TISSUE SPECIFICITY: OESOPHAGUS AND RUMEN. WEAKLY IN EPITHELIA AND
                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
MEDLINE; 92108053.
KOCH P.J., GOLDSCHMIDT M.
                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL ADHESION; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                  295 CIINIEDVNDNLP
                                                                                                                                          Local Similarity
                                                                           3 CNIKVKDVNDNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: FORMS 2A (SHOWN HERE) AND 2B ARE PROI
ALTERNATIVE SPLICING OF THE SAME GENE.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE
DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARDIAC MUSCLE.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00028; cadherin; 4. P09803; 1SUH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M81190; G163758; -. M81190; G163759; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOLDSCHMIDT M.D.,
                                                                                                                              Conservative
                                                                                                                                                                                   B
                                                                            15
                                                                                                    307
                                                                                                                                          53.1%;
CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOSKELETON;
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                                                                                                                           Score 60;
Pred. No.
3; Misma
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                                                                                                                                                                            K -> Q.

R -> Q.

K YOQCDONTH -> ESIRGHTLVKN (IN FORM MISSING (IN FORM 2B).

; 2173F06E CRC32;
                                                                                                                                                                                                                                                                                                     CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
                                                                                                                                                                                                                        POTENTIAL.
K -> Q.
R -> Q.
                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEMBRANE; REPEAT; ELETON; CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIMBELMANN R.,
                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC CADHERIN 1.
                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                              DESMOCOLLIN 2A/2B
                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                              Mismatches
                         896
                                                                                                                                          DB 1; I
2.61e-01;
                         8
                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                      Length 863;
                                                                                                                             Indels
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The bovine desmocollin family: a new gene and expression patterns reflecting epithelial cell proliferation and differentiation.";

J. CELL BIOL. 126:507-518(1994).

I. THE INTERACTION OF PLAQUE PROPEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS ESTWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.

I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

II TISSUE SPECIFICITY: STRATIFIED EPITHELIA ONLY (EPIDERMIS, TONGUE, DESCRIPAGUS AND ROWEN).
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE; 95403557.

YUE K.K.M., HOLTON J.L., CLARKE J.P., HYAM J.L.M., HASHIMOTO T.,

CHIDGEY M.A.J., GARROD D.R.;

"Characterisation of a desmocollin isoform (bovine DSC3) exclusively
expressed in lower layers of stratified epithelia.";

J. CELL SCI. 108:2163-2173(1995).
                                                                                                            REPEAT
                                                                                                                        DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                       PFAM; PF00028; cadi
HSSP; P09803; 1SUH
CELL ADHESION; GLY
                                                                                                                                                                                                                                                                                    EMBL; L33774; G914821; -. EMBL; L33774; G914822; -. EMBL; X75783; G433870; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).

-!- ALTERNATIVE PRODUCTS: FORMS 3A AND 3B ARE PRODUCED BY A SPLICING OF THE SAME GENE.

-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOS TAURUS EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESMOCOLLIN DSC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOMAIN: CALCIUM MAY BE BOUND BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GARROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARTIODACTYLA; RUMINANTIA;
                                                                                                 REPEAT
                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                          PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94308280
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                                                                                      DOMAIN
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEGAN P.K., YUE K.K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BOVINE).
METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
TA: RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
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                                                                                                                                                                                                                                       GLYCOPROTEIN;
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35, LAST ANNOTATION UPDATE)
 ROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL; CYTOSKELETON; CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIDGEY M.A.J., HOLTON J.L., WILKINSON R.W.,
KLHICNOD --
MISSING (II
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
VI -> EF ()
                                                                                                           CADHERIN 2.
CADHERIN 3.
                                                                                                                                   CYTOPLASMIC CADHERIN 1.
                                                                                      CADHERIN
                                                                                                CADHERIN
                                                                                                                                                              POTENTIAL
                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                     DESMOCOLLIN 3A/3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE CADHERIN-LIKE
                                                             (IN
 (IN REF.
                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3B ARE PRODUCED BY ALTERNATIVE
                                                            ESIRGHTG (IN FORM 3B).
                                                                                                                                                (POTENTIAL)
2)
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RESULT ACCOUNTS OF THE COLOR OF
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P52452;
01-OCT-1996 (REL. 3
01-OCT-1996 (REL. 3
01-NOV-1997 (REL. 3
                                        01-NOV-1997 (AMERICATION ORIGIN BINDAMA
REPLICATION ORIGIN BINDAMA
U73 OR CH6R.
U73 OR CH6R.
HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN Z29)
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERP
VIRUSES; DSDNA VIRUSES, ROSEOLOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997
01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WORMPEP; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARNORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
PUNROTTTUA: RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLE ARGINYL-TRNA (ARGRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
PFAM; PF00750; tRNA-SYNT_Id; 1.
AMINOACYL-TRNA SYNTHETASE; PROTEIN BIOSYNTHESIS;
SIMILAR 252 263 "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL FULTON L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
SEQUENCE FROM N.A. MEDLINE; 96195263. LINDQUESTER G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340
                                                                                                                                                                                                                                                                                                                                                                                                           375
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 52.2%;
Local Similarity 54.5%;
les 6; Conservative
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CATALYTIC ACTIVITY: ATP + L-ARGININE + TRNA(ARG) = AMP +

PYROPHOSPHATE + L-ARGINYL-TRNA(ARG).

SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNIKVKDVNDNFP
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9; Conser
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709 AA;
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                                                                                                                                                                                                                                                                            STANDARD;
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34, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
N BINDING PROTEIN (OBP).
INOUE N.,
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LAST SEQUENCE UPDATE)

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SYNTHETASE (EC 6.1.1.19)
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Pred. No. 4
4; Mismat
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1. No. 2.61e-01
Mismatches
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                                                                                                        HERPESVIRIDAE;
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CASTELLI J.W.
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Best Local S
Matches
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
REPLICATION ORIGIN BINDING PROTEIN (OBP)
U73 OR 19R OR HDPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Restriction endonuclease mapping and molecular cloning of herpesvirus 6 variant B strain Z29 genome.";
ARCH. VIROL. 141:367-379(1996).
-i- FUNCTION: PROBABLY INVOLVED IN DNA REPLICATION. BINDS OF REPLICATION (ORI) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBP_HSV6U
P52378;
                                                                                                                                      MEDLINE; 95266321.
GOMPELS U.A., NICHOLAS J.,
MARTIN M.E., EFSTATHIOU S.,
"The DNA sequence of human
and genome evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA REPLICATION; DNA-BINDING; ATP-BINDING.
NP_BIND 52 59 ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L14772; G405176; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAMEY F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                     conserved herpesvirus glycoprotein
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                      BETAHERPESVIRINAE; ROSEOLOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                  U73 OR 19R OR HDRFO.
HERPES SIMPLEX VIRUS (TYPE 6 /
VIRUSES; DSDNA VIRUSES, NO RNA
                                                                                                                                                                                                                  MEDLINE; 95146942.
LAWRENCE G.L., NICH
"Human herpesvirus
                                                                                        petween
                                                                                                                                                                                                                                                          SEQUENCE OF 1-703 FROM N.A.
                                                                                                                                                                                                                                                                                /IROLOGY
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                                                             European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                              EHV-1
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Similarity 53.3%;
8; Conservative
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                                                                                                                                                                                                      LAS J., BARRELL B.G.;
(strain UllO2) encodes homologues of the
s glycoprotein gM and the alphaherpesvirus
                                                                                                                                                                                                                                                                                                                      J., LAWRENCE G.,
U.S., CRAXTON M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TO FAMILY THAT GROUPS TOGETHER HSV-1
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Pred. No. 4.27e-01;
2; Mismatches 5
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STAGE;
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                                                                                                                                                                  REPLICATION.
                                                                                                                                          GROUPS TOGETHER
                                                                          There are no restrictions
                                                                                                                                                                                                                                                                                                                      JONES M., THOM MACAULAY H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                            structure,
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                                                                                          a collaboration -
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Best Local Similarity 53.3%;
Matches 8; Conservative
             EMBL; L33779; G1017465; -.
EMBL; L33779; G498019; -.
EMBL; X13885; G439671; -.
MGD; MGI:103221; DSC2.
MGD; MGI:103221; DSC2.
PROSITE; PS00223; CADHERIN; 3
PFAM; PP00028; Cadherin; 4.
HSSP; P09803; 1EDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSC2_MOUSE STAN
P55292; 064734;
01-0CT-1996 (REL.
01-0CT-1996 (REL.
01-NOV-1997 (REL.
DESMOCOLLIN 2A/2B E
                                                                                                                                                                                                                                                                                                                  JENKINS N.A., GILBERT D.J., COPELAND N.G.;

"MOUSE desmocallin (Dsc3) and desmoglein (Dsg1) genes are closely
linked in the proximal region of chromosome 18.";

GENOMICS 21:510-516(1994).

-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVE
IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL
POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: IN ALL EPITHELIA TESTED AND HEART.
-I- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                               modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSC2 OR DSC3.

MUS MUSCULUS (MOUSE).

EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; MAMMALIA;

EUKARYOTA; METAGOA; CHORDAE; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                     <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BUXTON R.S., WHEELER G.N., PIDSLEY S.C., MINISTER N.A., GILBERT D.J., COPELAND N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning, sequence analysis and expression desmocollin 2 (DSC2), a cadherin-like adhes MOL. MEMBRANE BIOL. 11:229-236(1994).
                                                                                                                                                                               use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 344-637 FROM N.A.
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DNA REPLICATION; DNA-BINDING; ATP-BINDING.
NP_BIND 52 59 ATP (POTENTIF
SEQUENCE 780 AA; 89716 MW; 5F096841 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORIMER J.E., HALL L.S., CLARKE J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95227276.
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                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: FORMS 2A AND 2B ARE PRODUCED E SPLICING OF THE SAME GENE.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS
                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                    DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produ
ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL;
                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                           non-profit institutions as long
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34, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
PRECURSOR (EPITHELIAL TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438
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Pred. No. 4.27e-01;
2; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pression pattern of mouse
ike adhesion molecule.";
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                                                                                                                                              (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                              28 ARE PRODUCED BY ALTERNATIVE
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CHAIN
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PROSITE; PS01230; TRMA_1; 1.
PROSITE; PS01231; TRMA_2; 1.
HYPOTHETICAL PROTEIN; HYDROLASE;
                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  modified and this statement
                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BADCOCK K., CHURCHER C.M., BARRELL B.G., RAJANDREAM N
SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: TO YEAST ENDO-EXONUCLEASE NUCR (RNC1)
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HYPOTHETICAL 59.6
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01-OCT-1996
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Q09833;
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SIGNAL
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ECPIATKTINEEXP
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Similarity 61.5%;
8; Conservative
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llarity 42.9%;
Conservative
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59613 MW;
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                                                    Score 58;
Pred. No.
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Pred. No. 4.27e-01;
2; Mismatches 3
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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DESMOCOLLIN 2A
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MISSING (IN FORM 2B).
37FE753B CRC32;
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CYTOPLASMIC
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                                                      ; DB 1; 1
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IN CHROMOSOME
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P41004;
01-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CAD5_MOUSE
P55284;
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EUKARYQTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME
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MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;

EUKARYOTA; METAZOA; CHORDATA; WORINAE;
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TISSUE-BRAIN CAPILLARY;

MEDLINE; 96141083.

BREIER G. BREVIARIO F., CAVEDA L., BERTHIER R., SCHNU
GOTSCH U., VESTWEBER D., RISAU W., DEJANA E.;

"Molecular cloning and expression of murine vascular ecadherin in early stage development of cardiovascular BLOOD 87:630-641(1996).
                                                                                                                                                                                                                                                                                                                                                                           CDH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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WAKA Y., SUTANI T., YAMASHITA Y., SAITOH S., YAMAUULA ...,
WAKASEKO Y., YANAGIDA M.;
WISSION YEAST CUt3 and Cut14, members of a ubiquitous protein
Wission Yeast cut3 and cut14, members of a ubiquitous protein
Wission Yearnived for chromosome condensation and segregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ## 11c ##
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LAST ANNOTATION UPDAT
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Pred. No. 6.94e-01;
4; Mismatches 4
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                                                                                                                                                                                                                                                                                   MAMMALIA; EUTHERIA; MUS.
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                                                                                                                           SCHNUERCH
                                                                    endothelial-
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                                                                                                                                                                                                                                                                                                                                                   CAD5_HUMAN P33151;
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CARBOHYD
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PFAM; PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:105057; CDH5.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                             01-OCT-1993 (REL. 27, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
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SEQUENCE FROM N.A.
TISSUE-ENDOTHELIAL CELLS;
MEDLINE; 95353875.
BREVLARIO F., CAVEDA L., CORADA M., MARTIN-PADURA I., NAVARRO BREVLARIO F., CAVEDA L., CORADA M., MARTIN-PADURA I., NAVARRO GOLAY J., INTRONA M., GULINO D., LAMPUGNANI M.G., DEJANA E.;
"Functional properties of human vascular endothelial cadherin
                                                                                                                                                       PRIMATES; CATARRHINI;
                                                                                                                                                                            EUKARYOTA;
                                                                                                                                                                                                  OMO
                                                                                                                                                                                                                                             (7B4 ANTIGEN) (CD144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 IRLEDINDNFP 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
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ADHESION; GLYCOPROTEIN;
                                                                                                                                                                              SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         x83930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.4%;
                                                                                                                                                                                                                                             ANTIGEN).
                                                                                                                                                         HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N: TYPE I MEMBRANE PROTE.
TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Œ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 1; L
Pred. No. 1.12e+00;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR POTENTIAL. CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CADHERIN
SER-RICH.
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VASCULAR E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.; DOB71215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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                                                                                                                                                                              VERTEBRATA; MAMMALIA; EUTHERIA
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                            OWOH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 783;
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DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
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SUZUKI'S., SANO K., TANIHAR

"Diversity of the cadherin

"tissue.";
                                                                                                                                       TRANSMEM
DOMAIN
REPEAT
                                                                                                                                                                                                  PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                         EMBL: X79981; G599834; -. EMBL; U84722; G1814076; -- EMBL; X59796; G29593; -. PIR: S24305; IJHUC5.
                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. CELL BIOL. 118:1511-1522(1992).

-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-!- THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGRINGOUS CELL TYPES. THIS CADHERIN MAY PLAY A IMPORTANT ROLE IN ENDOTHELLAL TYPES. THIS CADHERIN MAY PLAY A IMPORTANT ROLE IN ENDOTHELLA TYPES. THIS CADHERIN FOR THE CYTOSKELETON.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. FOUND AT CELL-CELL BOUNDARIES AND PROBABLY AT CELL-MATRIX BOUNDARIES.

-!- TISSUE SPECIFICITY: ENDOTHELIAL TISSUES AND BRAIN.

-!- SIMILARITY: BELONGS TO THE CADHERIN FORMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAMPUGNANI M.G., RESNATI M., RAITERI M., PIGOTT R., PISACANE HOUEN G., RUCO L.P., DEJANA E.;
"A novel endothelial-specific membrane protein is a marker of cell-cell contacts.";
                                                                         REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                            PFAM; PF00028; cadherin; 5. PFAM; PF01049; Cadherin_C_term; HSSP; P09803; 1EDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                        MIM; 601120; -. PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALI J., MULLER W.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                  CELL ADHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE
                                                                                                                       REPEAT
                                                                                                                                                                                     MAIN
                                                                                                                                                                                                                                                CALCIUM-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-ENDOTHELIAL CELLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL REGUL. 2:261-270(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 5-784 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (784/cadherin-5), an endothelium-specific cadherin.";
ARTERIOSCLER. THROMB. VASC. BIOL. 15:1229-1239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE: NAME-PROW; NOTE-CD guide CD144 entry; www-"http://www.ncbi.nlm.nih.gov/prow/cd/cd144.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92394977
                                                                                                                                                                                                                                                             GLYCOPROTEIN;
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adherin family:
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·
         CATOPLASMIC
CADHERIN 1.
CADHERIN 3.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
SER-RICH.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                             PHOSPHORYLATION;
                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                VASCULAR ENDOTHELIAL-CADHERIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            evidence for eight new cadherins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rmatics and the EMBL outst
There are no restrictions
ng as its content is in
                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                             TRANSMEMBRANE
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L outstation -
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Best Local Similarity
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ALTERNATIVE
SIGNAL
PROPEP
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            PARKER A. E., WHEELER G.N., ARNEMANN J., PIDSLEY S.C., ATALIOTIS P., THOMAS C.L., REES D.A., MAGEE A.I., BUXTON R.S.;
"THOMAS C.L., REES D.A., MAGEE A.I., BUXTON R.S.;
"Desmosomal glycoproteins II and III. Cadherin-like junctional molecules generated by alternative splicing.";
J. BIOL. CHEM. 266:10438-10445(1991).
-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLIN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENT MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERWAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSC2_HUMAN
Q02487;
Q1-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                                  PFAM; PF00028; cadherin; 4. HSSP; P09803; 1EDH. CELL ADHESION; GLYCOPROTEIN;
                                                                                                                                                   EMBL; X56807; G30508;
EMBL; X56807; G30509;
PIR; B40390; IJHUDA.
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                                                                                                                         PIR; A40390;
MIM; 125645;
                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         entities requires a
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HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (REL.
01-NOV-1997 (REL.
DESMOCOLLIN 2A/2B
                                                                                              PROSITE; PS00232; CADHERIN; PFAM; PF00028; cadherin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-KERATINOCYTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 IKVHDVNDNWP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESMOCOLLIN-3).
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                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
ALTERNATIVE PRODUCTS: TWO FORMS; 2A OR DGII DGIII; ARE PRODUCED BY ALTERNATIVE SPLICING SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                       DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                         NODES
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SPLICING; C

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136 901

136 694
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                                                                                                                                      IJHUDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442
523
535
517
87528 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28, CREATED)
28, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
PRECURSOR (DESMOSOMAL GLYCOPROTEIN II AND III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.4%;
                                                                                                                                                                                                                    license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                               ALT_INIT.
                                                     ROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL; CYTOSKELETON; CALCIUM-BINDING; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 1; I
Pred. No. 1.12e+00;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
I -> T (IN
V; C2C5CD71
DESMOCOLLIN 2A/2B.
EXTRACELLULAR (POTENTIAL)
                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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FT TRANSMEM 695 715 POTENTIAL.
FT DOMAIN 716 901 CATOPLASMIC (POTENTIAL).
FT REPEAT 144 355 CADHERIN 1.
FT REPEAT 344 355 CADHERIN 2.
FT REPEAT 472 579 CADHERIN 3.
FT REPEAT 472 579 CADHERIN 3.
FT REPEAT 34 34 POTENTIAL.
FT CARBOHYD 166 166 POTENTIAL.
FT CARBOHYD 546 546 POTENTIAL.
FT CARBOHYD 546 546 POTENTIAL.
FT CARBOHYD 546 546 POTENTIAL.
FT CARBOHYD 629 629 POTENTIAL.
FT CARBOHYD 629 629 POTENTIAL.
FT CARBOHYD 637 847 KVYLCNODENH -> ESIRGHTLIKN (IN FORM 2B/DGIII).
FT VARSPLIC 848 901 MW; CB688FC4 CRC32;
FT VARSPLIC 848 901 MMSSING (IN FORM 2B/DGIII).
SQ SEQUENCE 901 AA; 99961 MW; CB688FC4 CRC32;
Query Match
Best Local Similarity 53.8%; Pred. No. 1.12e+00;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db 341 CIINIDDVNDHLP 353
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Oy 3 CNIKVKDVNDNFP 15
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Search completed: Fri Jun 11 17:36:19 1999 Job time: 8 secs.

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MPsrch_pp protein · protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:36:36 1999; MasPar time 6.12 Seconds
133.859 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-5
Description: (1-15) from US08991628.pep

Sequence: 1 CECNIKVKDVNDNFP 15

Scoring table: PAM 150 Gap 15

searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mbc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 25.706; Variance 33.200; scale 0.774

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 9 8 8 7 6 5 5 4 4 3 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	ا سرر	Result No.
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VENTRAL MEDUAL CADHERI METHYLVIOLOGEN-REDUCIN RILAB: 7 PROTEIN. DNAJ PROTEIN. CO2D4.2 PROTEIN. SYNAPSIN S-SYN-SHORT (SYNAPSIN S-SYN-LONG (F DESMOCOLLIN TYPE 2 (FR REPLICATION ORIGIN-BIN SIMILARITY TO MULTIPLE MHC CLASS I PRECURSOR. INTESTINAL PEPTIDE-ASS LI-CADHERIN. PEPTIDE SYNTHETASE. DNA REPLICATION PROTEI CADHERIN. PERTICATION PROTEI CADHERIN. SIMILARITY SYNTHETASE. DNA REPLICATION PROTEI CADHERIN.5. KIDNEY-SPECIFIC CADHER ROSHIO.6 PROTEIN.		Description
6.34e.02 1.68e-01 1.68e-01 2.72e-01 2.72e-01 7.03e-01 7.03e-01 1.12e-00 1.12e+00 1.78e+00 1.78e+00 1.78e+00 1.78e+00 2.81e+00 2.81e+00 2.81e+00 2.81e+00		Pred. No.

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			•																					
MANNOSE 6-PHOSPHATE/IN	POLYPROTEIN (FRAGMENT)	MITOCHONDRIAL ATP9 GEN	VARIABLE MAJOR PROTEIN	TPH-TRYPTOPHAN HYDROXY	HYPOTHETICAL 206.5 KD	K12C11.4 PROTEIN.	POTASSIUM CHANNEL (FRA	493AA LONG HYPOTHETICA	B0281.8 PROTEIN.	G-CADHERIN.	CARBOXYPEPTIDASE GP180	CARBOXYPEPTIDASE D.	CADHERIN HOMOLOG.	T27E13.16 PROTEIN.	KSP-CADHERIN.	KIAA0345-LIKE 13.	CHAPERONE DNAJ.	296AA LONG HYPOTHETICA	HYPOTHETICAL 27.9 KD P	BETA4 - INTEGRIN.	BETA4 - INTEGRIN.	BETA4 - INTEGRIN.	INTEGRIN VARIANT BETA4	POTASSIUM CHANNEL (AKT
1.65e+01	1.65e+01	1.65e+01	٠	1.65e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	6.90e+00	6.90e+00			6.90e+00		6.90e+00	6.90e+00		6.90e+00	٠	4.42e+00	4.42e+00	4.42e+00	4.42e+00

ALIGNMENTS

8885		RESULT ID O	D V	ма Ма	SQ		CPP	R R R	2888		RESULT
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES; SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;	01-JUN-1998 (TREMBLREL, 06, CREATED) 01-JUN-1998 (TREMBLREL, 06, LAST EQUENCE UPDATE) 01-JUN-1998 (TREMBLREL, 06, LAST ANNOTATION UPDATE) HYPOTHETICAL 25.1 KD PROTEIN C16E8.02 IN CHROMOSOME I.	13737 PRELIMINARY;	251 CECSIKIKDVNDNFP 265 : : :	Query Match 94.7%; Score 107; DB 11; Length 993; Best Local Similarity 86.7%; Pred. No. 4.84e-12; Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	NON_TER 993 993 SEQUENCE 993 AA; 107888 MW; 881794BD CRC32;	2290200; (2; CADHERIN; 2. (cadherin; 4. (croppostu. Transcrepts and.	ISHIKAWA H., LI K., UITTO J.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS	IL J SEQUENCE FROM N.A. STRAIN-BALB/C;	NUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	035902; 01-JAN-1998 (TREMBLREL. 05, CREATED) 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DESMOGLEIN 3 (FRAGMENT).	T 1 035902 PRELIMINARY; PRT; 993 AA.

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RESULT

ID Q90425

AC Q90425;

C Q90425;

DT 01-NOV-1996 (TREMBLREL 01, CREATED)

DT 01-NOV-1996 (TREMBLREL 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)

DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)

DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)

DE VENTRAL MEURAL CADHERIN (FRAGMENT).

C EUKARYOTA; METAZOA; CHORDATA; VERTEBERATA; ACTINOPTERYGII, NEOPTERYGII

OC CYPRINIDAE; METAZOA; CHORDATA; VERTEBERATA; ACTINOPTERYGII, NEOPTERYGII

OC CYPRINIDAE; RASBORINAE; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;

KN (1)

RP SEQUENCE FROM N.A.

FRANKLIN J.L., SARGENT T.D.;

RL DEV. DYN. 2060-0(0).

RL DEV. DYN. 2060-0(0).

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

DR PROSITE; U41419; G1345125; ...

DR PROSITE; PS00232; CADHERIN; 1.

DR PFAM; PF00028; CAGHERIN; 1.

DR PFAM; PF01049; Cadherin; 3.

DR PFAM; PF01049; Cadherin; 3.

DR PFAM; PF01049; Cadherin; 3.

DR PFAM; PF01049; Cadherin; 1.

FI NON_TER

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SCCUENCE 519 AA; 57807 MW; E6DA0079 CRC32;
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HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
I TRANSMEM 28 48 POTENTIAL.
I TRANSMEM 31 34 POLY-LEU.
T TRANSMEM 66 86 POTENTIAL.
T TRANSMEM 106 126 POTENTIAL.
T TRANSMEM 136 156 POTENTIAL.
T TRANSMEM 136 156 POTENTIAL.
T TRANSMEM 136 25122 MW; CE8F8E6B CRC32;
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Best Local S
Matches 1
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Best Local S
Matches
                                                                                      Q58593 PRELIMINARY;
Q58593; QTREMBLREL, 07,
Q1-AUG-1998 (TREMBLREL, 07,
Q1-NOV-1998 (TREMBLREL, 08,
METHYLVIOLOGEN-REDUCING HYI
VHUB OR MJ1193,
METHANOCOCCUS JANNASCHII.
ARCHAEA; EURYARCHAEOTA; METHANOCOCCUS.
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STRAIN-972;

OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WOOD V.;

SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)

-I- SIMILARITY: TO YEAST YGLOLOW AND SOME, TO N.CRASSA ATP-6.
   SEQUENCE FROM N.A STRAIN-DSM 2661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHIZOSACCHAROMYCES [1]
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|||:||| :|:|
4 NIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 NIKVKDVNDNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 57.5%;
Similarity 91.7%;
11; Conservative
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8; Conservative
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07, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
HYDROGENASE POLYFERREDOXIN PROTEIN.
                                                                                                                       METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
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No. 6.34e-02;
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CPIGIKKVDDDFP CNIKVKDVNDNFP

95

Query Match Best Local S Matches

Similarity

55.8%; larity 53.8%; Conservative

Score Pred. 3; M

re 63; DB 1; I 1. No. 1.68e-01; Mismatches 3

Length 394;

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Gaps

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MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHWANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAYAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., WERRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEILDWAN J.F., FUHRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW F.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschil.", SCIENCE 273:1058-1073(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
-!- THIS PROTEIN CONTAINS SEVERAL REPEATED FERREDOXIN-LIKE DOMAINS.
-!- COFACTOR: BINDS TEN 4FE-48 CLUSTER.
-!- SUBUNIT: VHU CONSISTS OF THE VHUA, VHUG, VHUU SUBUNTS AND A FERREDOXIN PROTEIN.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               ELECTRON
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AA,
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43342
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RESULT 5
ID Q21920;
AC RASDIIN
RA SEQUENC
RA WALLON
RA GARNNE!
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RA GARNIN
RA GARNIN
RA GUMMIN
RA CUMMIN
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RA CUMMIN
RA EMBL;
DR EMBL;
STRAIN-NO.7;

X MEDLINE; 97214635.

A MOMMA K., INUI M., YAMAGATA H., YUKAWA H.;

XT "Cloning of dnak and dnaJ homologous genes fro

RT bacterium Rhodopseudomonas species.";

RL BIOCHIM. BIOPHYS. ACTA 1350:235-239(1997).

RC C:-:-SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AN

CC DNAJ-LIKE PROTEINS.

CC DNAJ-LIKE PROTEINS.

CC EMBL; D78133; D1020582; -.

CR EMBL; D78133; D1020582; -.
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Best Local :
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MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILSON R., AINSCOUGH R., CONNEIL M., COPSEY T., COOPER J., COULSON A. BONFIELD J., BURTON J., COURBIN R., FAVELLO A., FULTON L., CARATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., CARATON M., DEAR S., DU Z., DURBIN T., LAISTER M., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN DARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN J. SANLDON M., SNITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997
01-JUL-1997
01-NOV-1998
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EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q21920; Q21927;
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                       RHODOPSEUDOMONAS SP. BACTERIA; PROTEOBACTERIA;
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270310; E1348745; JOINED.

270310; E1348615; -1.

270686; E1348615; JOINED.

JENCE 2606 AA; 285415 MW;
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7; Conser
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(TREMBLREL.)
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                                                                                                                                                                                                                                                                                                                                                                                                                       SUBDIVISION; BRADYRHIZOBIUM GROUP;
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CORATTON M., DEAR S., DU 2., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THLERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00637; DNAJ_CXXCXGXG; PRAM; PF000226; DNAJ_CXXCXGXG; 1. CHAPERONE; DNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 368:32-38(1994).

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY EMBL; Z81031; E1343679; -. PROTEIN_RECEPTOR; 1.

G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN SEQUENCE 501 AA; 56404 MM; 18F1C57F CRC32;
                                                                                                                                                                                                          076322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHAN
                                         LOLIGO PEALEII (LONGFI)
EUKARYOTA; METAZQA; MOJ
MYOPSIDA; LOLIGINIDAE;
                                                                                                            01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
SYNAPSIN S-SYN-SHORT (FR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 94150718.
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01-JUL-1997
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                                                        S-SYN-SHORT (FRAGMENT).
EALEII (LONGFIN SQUID).
A: METAZQA; MOLLUSCA; CEPHALOPODA; COLEOIDEA; TEUTHOIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A
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(TREMBLREL.)
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A REPLICATION.
9 AA; 40992 MW;
                                                                                                                                                                                                                                                                                                                                                                                346
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38.5%;
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Pred. No. 2.72e-01;
5; Mismatches 0
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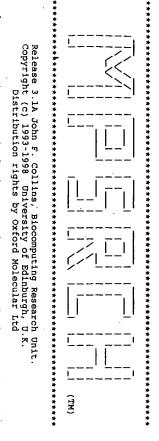
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01-NOV-1998
01-NOV-1998
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O76323;
O1-NOV-1998 (TREMBLREL. 08, CREATED)
O1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
           EUR. J. CELL BIOL. 76:192-203(1998).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PREMBL; AJ002299; E1315148; -.
PROSITE; PS00232; CADMERIN; 3.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE;
                                                                                                                                                                                                                                                     CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA; VI
CARNIVORA; FISSIPEDIA; CANIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 98380123.
ROBERTS G.A., BURDETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Two Sites of Action for S
Neurotransmitter Release."
SUBMITTED (MAR-1998) TO EN
EMBL; AF055374; G3273726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. HILFIKER S., SCHWE AUGUSTINE G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNAPSIN S-SYN-LONG (FRAGMENT).
LOLIGO PEALEII (LONGFIN SQUID).
EUKARYOTA; METAZOA; MOLLUSCA; CEPHALOPODA; COLEOIDEA;
MYOPSIDA; LOLIGINIDAE; LOLIGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Two Sites of Action for Synapsin Domain E Neurotransmitter Release."; SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ EMBL; AF055373; G3273724; -.
                                                                                                                     "Antisense expression of a desmosome plaque assembly he
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                                                                                                                                                                R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 53.1%;
Similarity 35.7%;
5; Conservative
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(TREMBLREL.
                                                                                                                                                                                                                                                                                                                                 TYPE
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larity 35.7%;
Conservative
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                                                      BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULS CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATEFILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN I PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKI SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON B., WATERON D., WATERSTON B., WATERON A., WEINSTOCK I., WITTERSTON VAUGHAN K., WATERSTON B.
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STRAIN-BRISTOL N2;
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WILSON R., AINSCOUGH I
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
DU Z., GATTUNG S.;
SUBMITTED (MAY-1997) [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P79570;
P79570;
                  LT 14
012864
012864
012864;
01-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
101-NOV-1998 (TREMBLEL 08, LAST ANNOTATION UPDATE)
INTESTINAL PEPTIDE-ASSOCIATED TRANSPORTER HPT-1.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAROA; CHORDATA; VERTEBRATA; MANMALIA;
                                                                                                                                                                                                                                                                                  KATAGIRI T., HIRONO I., AOKI T., SAKAI M.;
"Isolation of major histocompatibility com,
salmon (Oncorhynchus gorbuscha).";
DEV. COMP. IMMUNOL. 20:217-228(1996).
EMBL; D58386; D1010196; -.
PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1629 CKCHVIVLDENDNLP 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  II. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILAN EMBL; AF003388; G2088652; -. PROSITE; PS00232; CADHERIN; 8
PFAM; PF00028; cadherin; 14.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; SEQUENCE 2163 AA; 238609 MW; 6C85C652 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                               ONCORHYNCHUS GORBUSCHA (PINK SALMON) (HUMPBACK SALMON).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (MAY-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
            CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                         SIGNAL; MHC.
                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97113756.
KATAGIRI T., HIRON
                                                                                                                                                                                                                                                                                                                                                                                                                      NCORHYNCHUS.
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                                                                                                                                                                                                                                                                                                                                                                                  ISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 52.2%;
Local Similarity 53.3%;
les 8; Conservative
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Similarity 38.5%;
5; Conservative
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339 AA;
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(TREMBLREL. 03,
(TREMBLREL. 09,
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38268 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.12e-
3; Mismatches
                                                                                                                                                                                                                Score 58; |
Pred. No. 1
                                                                                                                                                                                                    5; Mismatches
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PROTEIN (BY
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Best Local S
Matches
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JENKINS I.L., DUCKNORTH D.C., SPORTSMAN R., MACKENSEN D.,
A JENKINS I.L., DUCKNORTH D.C., SPORTSMAN R., MACKENSEN D.,
A ROSTECK P.R., SKATRUD P.L.,
I "Association of intestinal peptide transport with a protein relation the cadherin superfamily.";
I SCIENCE 264:430-433(1994).
C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY.)
C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY.)
PROSITE, PS00232; CADHERIN; 3.
PROSITE, PS00232; CADHERIN; 3.
PROSITE, PS00232; CADHERIN; 3.
PROSITE, PS00232; CADHERIN; TRANSMEMBRANE; CALCIUM-BINDING; REP.
SEQUENCE 832 AA; 92147 MW; B5193483 CRC32;
                                                               Query Match
Best Local
                                                    Matches
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Q15336
Q15336;
                                                                                                                                                                     SEQUENCE FROM N.A.
BOETTINGER A., KREFT B., FIEGER C., DLOUHY
GOESSNER R., TAUBER R.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
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                                                                                                        PFAM; PF00028; cadherin; 6.
CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; SEQUENCE 832 AA; 92207 MW; 65C92D4C CRC32;
                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                             EMBL; X83228; G854175; -. PROSITE; PS00232; CADHERIN; 3.
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                                                                                                                                                                                                                                                                                               LI-CADHERIN
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                          325 EIHVKVKDINDNPP 338
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 ECNIKVKDVNDNFP
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                                                   h 51.3%;
Similarity 64.3%;
9; Conservative
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(TREMBLREL.)
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                                                  Score 58; DB 4; L
Pred. No. 1.78e+00;
3; Mismatches 2
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.78e+00;
3; Mismatches 2
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PROTEIN (BY
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                                                                            Length 832;
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                                                      Indels
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Search completed: Fri Jun 11.17:38:42 1999 Job time: 126 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:45:41 1999; MasPar time 7.95 Seconds 40.150 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: 109 >US-08-991-628-6
(1-15) from US08991628.pep

Sequence: SARTLNNRYTGPYTF 15

Scoring table:

PAM 150 Gap 15

170751 segs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

geneseq35

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7: 8:part8 9:part9 10:part10 11:part11 12:part12 13:p 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part22 23:part22 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 :part39 13:part13

Mean 19.152; Variance 58.684; scale 0.326

Statistics:

Pred. No. score grea greater t is the number of ter than or equal than or equal to the score by analysis of the total results predicted by chance to have a to the score of the result being printed,

Result No.	Score	Query	Length	B	ID .	Description	Pred. No.
1			15	20	W04846	Self epitope of desmo	5.33e-05
N		100.0	614	19	W07908	higus vulga	•
ω			999	σ	R30742	phiqus	
4	56		480	N	R12099	Haem 84-2 portion of	6.15e+01
5			516	N	R12098	84-1 portion	6.15e+01
o			431	17	R97293	Mouse CRF RB1 recepto	7.81e+01
7		49.5		ω	P61040	nO.	9.89e+01
80				œ	R40924	Protein able to bind	9.89e+01
9				22	W08609	Chimeric MoMLV and Ty	
10			429	22	W08606		
11				15	R90575		9.89e+01
12	54		449	22	W08608	Chimeric MoMLV and Ty	٠
13	54	49	1196	16	R75189		
14	53		105	21	W00832	Variable light chain	1.25e+02
15	53			24	W19018	Anti-human FasL antib	1.25e+02
16	53		653	7	R37425	IDUA.	1.25e+02

45	44	43	42	41	40	39	38	37	36	<u>ა</u>	34	u u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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W17899	W56573	W68155	W56579	R32074	W46621	R54013	R70256			2	W72435	W06447	R28751	R25413	R39567	R25254	R25101	W56557	W17871	W18302	W56558	R04711	R97842	4.1	N. 3	W52241	10	10
rhabdus 1	Toxin TcdAii, encoded	Human angiotensin con	Fragment of toxin Tcd	Bovine transglutamina	Amino acid sequence o	S	t b	Humanised HP1/2 light	Transplanted VK seque	ted	VK S	VL re	Light chain variable	chain	ence of t		prodrug	Toxin TcbA, encoded b	Photorhabdus luminesc		bAii,	Sequence of guinea pi	Ō.	sarcoma a:	LD1/2-6-3:	LD1/2-6-3	us rubella	н
.99e+0	.99e+0		. 99	.99e	1.99e+02	.99e+0	1.99e+02	9e+0	.99e+0	.99e+0	.99e+0	. 996	. 99	1.99e+02	.99e+0	1.99e+02	.99e+0	5	.58e+0	•	1.58e+02	. 58	.58e+0	.58e+0	5	8e	25	. 23

ALIGNMENTS

derived from th polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II protein, such as HLA-DR, which is associated with a human autoimmune disease and which binds to the polypeptide to activate autoreactive T-cells in individuals with the autoimmune disease. This peptide is derived from the human desmoglein 3 protein (amino acids 512-526) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein protein are described in W04841-47. Claim 1; Page 41; 58pp; English.

Claim 1; Page 41; 58pp; English.

Pharmaceutical preparations for tolerisation to antigens comprise either an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid polypeptide (whether self or non-self) includes an amino acid Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in Strominger JL, WW WPI, 96-425218/42 12-SEP-1996. 07-MAR-1996; U03182. 07-MAR-1995; US-400796. (HARD) HARVARD COLLEGE л 1 W04846 standard; peptide; 15 AA auto-immune disease autoantigen; HLA; human leukocyte antigen; T-cell; pemphigus vulgaris; desmoglein; multiple sclerosis; Self epitope of desmoglein 3, implicated in autoimmune disease Tolerisation; self-epitope; antigen; autoimmune disease; numan papili nerpes simplex virus; adenovirus; phosphomannomutase; numan papillomavirus; Epstein-Barr virus; DNA polymerase; 18-FEB-1997 (first entry) haemagglutinin; Wucherpfennig KW sigma protein thymocyte; an

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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27-NOV-1991; 798918.
27-NOV-1991; US-798918.
(USSH ) US DEPT HEALTH & HI
Amagai M, Klaus-kovtun V,
WPI; 93-067436/08.
N-PSDB; Q35992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-1996.
30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris claim 1; Page 7-9; 9pp; Japanese.

W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgGl hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                               DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English. This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R30742
R30742;
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Autoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W07908 standard;
W07908; ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J08188540-A.
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Similarity 100.0%;
15; Conservative
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Score 109; DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R12099;
                                                                                                                                  Protein from Haemonchus contortus and other nematodes - used as therapeutic and prophylactic agent to protect plants, animals or humans from parasitic nematode infection.

Disclosure; Fig 49; 209pp; English.

The proteins derived from the nematode DNA may be used to derive vaccines against parasitic infection of plants, humans and animals esp. sheep. MAbs may also be raised to provide passive therapy and Sequence 516 AA;
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01-MAR-1990; US-487181.
(SYNE-) SYNERGEN INC.
WPI; 91-133285/19.
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Parasitic nematode; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1991.
17-SEP-1990; 062569.
18-SEP-1989; US-408339.
01-MAR-1990; US-487181.
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Mismatches 3;
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                                                                                                                                                                                           mouse heart library. Recombinant mCRF-RBI can be expressed in host cells transformed by the CDNA clone. The receptor can be to identify agonists and antagonists that modulate the signal transduction activity mediated by CRF receptors. It may be administered therapeutically to reduce high ACTH levels caused
                                                                                                                                                                                                                                                                                                                                                     13-JUN-1996.
06-DEC-1995; U15909.
09-DEC-1994; US-353537.
17-JAN-1995; US-374009.
(SALK ) SALK INST BIOLOGICAL STUDIES.
Chen R, Donaldson CJ, Lewis KA, Perrin
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21-AUG-1996
                    P61040 standard; Protein;
P61040;
03-JUL-1991 (first entry)
                                                                                                                                                                                                                                Mouse corticotropin releasing factor receptor mCRF-RB1 was identified as the product of a CDNA clone (T28972) isolated mouse heart library. Recombinant mCRF-RB1 can be expressed host cells transformed by the cDNA clone. The receptor can
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N-terminal region of bacterial expression vector. Galactose; expression vector.
                                                                                                                                                                                                                                                                           Claim 3; Page 83-85; 102pp;
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by CRF-R
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levelop prods. for modulating signal transduction
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                                                                                      RTLNNRYTGPYTF
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16-JUL-1997 (first entry)
16-JUL-1997 (first entry)
16-JUL-1997 (first entry)
Chimeric MoMLV and Ty3 integrase designated AtBmCm.
Chimeric MoMLV and Ty3 integrase designated AtBmCm.
MoLoney murine leukaemia virus; Saccharomyces cerevisiae;
MoLoney murine leukaemia virus; Saccharomyces cerevisiae;
retrotransposoni "yeast Ty3; position specific integration;
inflammation; cardiovascular; autoimmune; cancer; HIV; haemophilia;
inflammation; cardiovascular; autoimmune; cancer; HIV; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzyme expression vector - giving transformant enzyme be used as host enzymes in polypeptide biosynthesis. Disclosure; Fig 4; 12pp; Japanese.
The vector may be used to express heterologous genes transformed host when galactose is added as a carbon Sequence 91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1985.
23-MAY-1984; 102685.
23-MAY-1984; JP-102685
                                                                                                                                                                                                                                                                                  The synthetic gene encodes a protein corresponding to an antibody capable of binding to a specific antigen, in this case the HIV-1 tat protein. Many synthetic genes are synthesised, each containing a predetermined nucleotide region encoding the framework regions of the heavy and light chains of antibody and undetermined nucleotide regions which are random sequences. The genes are then used in the construction of vectors which are subsequently used to transform microbes. The proteins thus produced are screened for binding activity to the specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R40924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIS ) SHISEIDO KK. WPI; 86-025462/04.
                                                                                        W08609;
                                                                                                                                                                                                                                                                                                                                                                                                             disease diagnosis, etc.
Claim 13; Page 22; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-1992; US-843125.
(HOFF ) HOFFMANN LA ROCHE
Dillon PJ, Rosen CA;
WPI; 93-274375/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen-binding proteins and constructed synthetically and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies; antigen binding proteins; library; Human Immunodeficiency Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; Q48605
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                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein able to bind to HIV-1 tat
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                                                                                                                                                                                      57 arvldgsingryti 70
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                                                                                                                                                            ARTLNNRYTGPYTF
                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                  h 49.5%;
Similarity 42.9%;
6; Conservative
                                                                                                                                                                                                                                                                        246 AA;
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llarity 54.5%;
Conservative
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Pred. No.
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Pred.
3; N
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                                                                                                                                                                                                                                 54; DB 8;
No. 9.89e+01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                           Length 246
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Best Local :
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10-MAY-1996; U05727.

10-MAY-1996; US-445466.

(CHIR) CHIRON VIAGENE INC.
(REGC) UNIV CALIFORNIA.

Bilachone VW, Dildine SL,
                                                                                                                                                                                                                              W08666;
16-UUL-1997 (first entry)
Chimeric MOMLV and Ty3 integrase designated AmBtCm.
Chimeric MOMLV and Ty3 integrase designated AmBtCm.
Moloney murine leukaemia virus; Saccharomyces cerevisiae;
Moloney murine leukaemia virus; Saccharomyces cerevisiae;
retrotransposon; yeast Ty3; position specific integration;
retrotransposon; yeast Ty3; position specific integration;
                                                                                                                                                                       Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector construct into a defined region of a target eukaryotic genome. As part of gene delivery vehicles and transduction competent recombinant retroviral particles it can be useful in somatic and germ cell gene therapy (in vivo or ex vivo) of a wide range of genetic, infectious, degenerative, inflammatory, cardiovascular and autoimmune diseases or cancer. Typical examples of the many potential applications include treatment of HIV infection, haemophilia, Alzheimer's disease and rheumatoid arthritis. This protein rather than wild-type retroviral integrase reduces the rate of insertional mutagenesis and the degree of variation in gene expression, and particularly does not disrupt
                                                                                                                                                                                                                                                                                                                                                                T 10
W08606 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tRNA gene expression.
N.B. The present sequence is made up from the two original
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a specific example of a chimeric integrase made up of three domains from MOMLV and Ty3, with at least one domain derived from Ty3 integrase. This protein can direct integration of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New chimeric integrase for targetted eukaryotic genomes - useful for gene
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Claim 7; Page -; 98pp;
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                                                                                                                                   domain
                                                                                                                                                         Кey
                                                                                                                                                                                                                 Alzheimer's disease; rheumatoid arthritis; chimeric
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    Moloney murine leukaemia virus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                              /note= "From 42..284
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/note= "From MoMLV"
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                        "From
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "From MoMLV"
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l sequences as
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No. 9.89e+01;
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therapy, providing
rates of insertion
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Claim 7; Page -; 98pp; English.

The present sequence is a specific example of a chimeric integrase made up of three domains from MoMLV and Ty3, with at least one domain derived from Ty3 integrase. This protein can direct integration of a vector construct into a defined region of a target eukaryotic genome. As part of gene delivery vehicles and transduction competent recombinant retroviral particles it can be useful in somatic and germ cell gene therapy (in vivo or ex vivo) of a wide range of genetic, infectious, degenerative, inflammatory, cardiovascular and autoimmune diseases or cancer. Typical examples of the many potential applications include treatment of HIV infection, haemophilia, Alzheimer's disease and rheumatoid arthritis. This protein rather than wild-type degree of variation in gene expression, and particularly does not disrupt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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eukaryotic genomes - useful for gene
consistent gene expression and lower
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Sandmeyer SB;
WPI; 97-021229/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tRNA gene expression.

N.B. The present sequence is not shown in t made up from the two original sequences as which are shown.
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22-MAY-1995; US-445466.
(CHIR ) CHIRON VIAGENE INC.
(REGC ) UNIV CALLFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebrovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRF2-beta receptor;
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Local Similarity 46.2%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRF2-beta receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARTLNNRYTGPYT
                                                                                                                                                                                                                                                                                                                                                                                                            sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein; 431
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                                                                                                                                                                                                                                                                                                                                                                                                                               disorder; memory
                                                                                              /labei
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/note= "From MoMVL"
                                                          /label=
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                                                                                                                                         'labe
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                                                                                                                                                                                                                                                                                                                                                  'label- Extracellular_N-terminal_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 corticotropin-releasing factor-2 receptor; order; memory disorder; Alzheimer disease.
                                                                                                                                                                                                                                                                                                                                138
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                                                                                                                                       Transmembrane_domain
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therapy, providing more
rates of insertional
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9.89e+01;
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Best Local s
Matches
                                    28-NOV 1996.
28-NOV 1996; U06727.
10-MAY-1995; US-445466.
22-MAY-1995; US-445466.
(CHIR ) CHIRON VIAGENE INC.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09534651-A2.
21-DEC-1995.
14-JUN-1995;
14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric MoMLV and Ty3 integrase designates cerevisiae;
Moloney murine leukaemia virus; Saccharomyces cerevisiae;
retrottansposon; yeast Ty3; position specific integration;
retromation: cardiovascular; autoimmune; cancer; HIV; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W08608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (R90575) is a membrane-bound G-coupled protein receptor involved in signal transduction. It can be produced by expression of encoding cDNA (T12244) in procaryotic or eucaryotic host cells. Recombinant CRF2 receptor is used to screen CRF2 receptor agonists and antagonists of therapeutic appln., and to prepare antibodies which specifically bind to CRF2 receptors.
Bilachone VW, Di
Sandmeyer SB;
WPI; 97-021229/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 63-66; 109pp; English.
Rat corticotropin-releasing factor-2-beta (CRF2-beta) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to isolate CRF-2 receptor antagonists for t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corticotropin-releasing factor-2 receptor, and DNA encoding it used to isolate CRF-2 receptor antagonists for the treatment of remembrovascular disorders, memory disorders and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T12244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-1995; U07757.
14-JUN-1994; US-259959.
31-JAN-1995; US-381433.
07-JUN-1995; US-485984.
(NEUR-) NEUROCRINE BIOSCIENCES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae transposon Ty3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moloney murine leukaemia virus
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1, Oltersdorf T;
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343..363
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310..329
                                                                                                                                                                                                                                                    /note= "F
305..449
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/note From Ty3"
62..304
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                                                                                                                                                                                                           /label= C
/note= "From MoMLV"
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Pred. No. 9.
                                           Jolly DJ,
                                                                                                                                                                                                                                                                              ТУ3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Å
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9.89e+01;
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Matches
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05-APR-1994; 411718.
05-APR-1994; DE-411718.
05-APR-1994; DE-411718.
(GSFU-) GSF FORSCHUNGSZENTRUM UMWELT
(GSFU-) GSF Wheel W, Oestergaard M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a Specific example of a chimeric integrase made up of three domains from MoMLY and Ty3, with at least one domain derived from Ty3 integrase. This protein can direct integration of a vector construct into a defined region of a target eukaryotic genome. As part of gene delivery vehicles and transduction competent recombinant retroviral particles it can be useful in somatic and germ cell gene therapy (in vivo or ex vivo) of a wide range of genetic, infectious, degenerative, inflammatory, cardiovascular and autoimmune diseases or cancer. Typical examples of the many potential applications include treatment of HIV infection, hemophilia, Alzheimer's disease and rheumatoid arthritis. This protein rather than wild-type retroviral integrase reduces the rate of insertional mutagenesis and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tRNA gene expression.

N.B. The present sequence is not shown in the specification, but is N.B. The present sequence is not shown in the specified, MOMLV and Ty3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutagenesis
Claim 7; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New chimeric integrase for targetted vector integration in
eukaryotic genomes - useful for gene therapy, providing mo
consistent gene expression and lower rates of insertional
1131 tknleprwkgpyt 1143
                                                                                                                                                      The full-length proviral genomic sequence of retrovirus RPB-14 has been determined. The virus codes for an osteoinductive protein, although the precise location of the coding region has not yet been identified. The virus may be useful in gene therapy of bone growth
                                                                                                                                                                                                                                                                           Erfle V, Gimbel W,
Schmidt J, Strauss P;
WPI; 95-352078/46.
                                                                                                      disorders such as osteoporosis. viral pol gene product. Sequence 1196 AA;
                                                                                                                                                                                                                           RFB-14 retrovirus genome - ar
Claim 14; Fig 1; 46pp; German.
                                                                                                                                                                                                                                           RFB-14
                                                                                                                                                                                                                                                             N-PSDB; Q94266.
                                                                                                                                                                                                                                                                                                                                                                                                     DE4411718-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                    Retrovirus RFB-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                       reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFB retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osteoinductive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R75189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          degree of variation in gene expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 tknleprwkgpyt 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ARTLNNRYTGPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 1196 AA.
                                h 49.5%;
Similarity 46.2%;
6; Conservative
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larity 46.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  retrovirus RFB-14 pol gene product.
; gag; pol; env; osteogenesis; osteoinductive protein;
nt; osteoporosis; gene therapy; polymerase;
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                                Score 54;
Pred: No.
3; Misma
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Pred. No. 9.89e+01;
3; Mismatches 4
                                                                                                                                                                                                                                           and prodn.
                                                                                                                                      The present sequence is that of the
                                   No. 9.89e-
Mismatches
                                                                                                                                                                                                                                                                                                                 Pedersen
                                                                                                                                                                                                                                                                                                               GESUNDHEI.
Pedersen FS,
                                                    DB 16;
9.89e+01;
                                                                                                                                                                                                                                           of osteo-inductive proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and particularly does not disrupt
                                                                  Length 1196;
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                                   Gaps
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RESULT 14 ID W00832: AC W00832;

standard; Protein; 105 AA

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ARTLNNRYTGPYT

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Pl solution

PS Claim 28; Page 91; 133pp; Japanese.

CC The present sequence is the light chain variable region of the great the sequence is the light chain variable region of the present sequence is the light chain variable region of the grant human Fas ligand monoclonal antibody (WAB) NOK-5 NOK-5 is produced by the hybridoma NOK-5 (FERM BP-5048), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma P3x63Ag8 653 (ATCC CRL-1580) cells. The MAB recognises the human CC Fas ligand on the cell surface or in solution, and can be used to inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay in CC biological samples (e.g. human blood), especially for disease CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic CC lupus erythematosis.

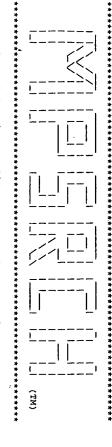
So Sequence 105 AA;
                  RESOLUTION OF THE SOLUTION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches
Anti-human Fas Ligand antibody to treat hepatitis - controls apoptosis in liver cells and improves liver function Claim 6; Page 41; 51pp; Japanese.

The present sequence is the light chain variable region of the murine anti-human Fas ligand (FasL) monoclonal antibody (MAb) NOK5, which is expressed by the hybridoma NOK5 (FERM BP-5044). The MAb can be used in the preparation of a composition for the effective oral or parenteral treatment of hepatitis, including hepatitis caused by hepatitits B or C virus. The composition controls apoptosis in liver cells caused by the binding of FasL to Fas expressing liver cells, and improves liver function by improving blood glutamate oxaloacetate and pyruvate transaminase levels. The composition is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-1998 (first entry)
Anti-human Fasi antibody (NOK5) light chain variable region.
Light chain; variable region; mouse; murine; human; Fas ligand;
Fasi; monoclonal antibody; MAb; hybridoma; treatment; hepatitis;
hepatitis; B virus; HBV; hepatitis C virus; HCV; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUME ) SUMITOMO ELECTRIC IND CO.
Kayagaki N, Nakata M, Okumura K
WPI; 96-443140/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variable region; light chain; human; Fas ligand; monoclantibody; NOK-5; hybridoma; inhibition; apoptosis; assadiagnosis; disease; hepatitis; infectious mononucleosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUME ) SUMITOMO ELECTRIC IND CO. Kayagaki N, Nakata M, Okumura K, WPI; 97-258767/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997.
24-OCT-1996; J03089.
27-OCT-1995; JP-303491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
WO9715326-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T39558
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27-OCT-1995; JP-303492.
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Variable light chain of anti-human Fas ligand antibody NOK-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T69542
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Local Similarity 62.5%;
Local Similarity 
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Pred. No. 1.25e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yagita H;
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                                                                      Query Match
Best Local
                                                        Matches
                                                                                                                         were fused with mouse myeloma cells to produce hybridomas. The hybridomas were screened for anti-FasL activity, and the active clones NOKI-5 isolated.
                                                                                                                                                                 given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day. Spleen cells from mice immunised with Fast expressing COS cells
                                                                                                               Sequence
91 hysspytf 98
:|::|||
8 RYTGPYTF 15
                                                     / Match 48.6%;
Local Similarity 62.5%;
les 5; Conservative
                                                                                                               105 AA;
                                                     Score 53;
Pred. No.
3; Misma
                                                        Mismatches
                                                                   ; DB 24; I
. 1.25e+02;
                                                         0
                                                                                   Length
                                                         Indels
                                                                                   105
                                                         0
                                                      Gaps
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Search completed: Fri Jun 11 17:50:17 1999 Job time: 276 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Jun 11 17:50:33 1999; MasPar time 4.35 Seconds 138.311 Million cell updates/sec

Title: Description: Perfect Score: Sequence: >US-08-991-628-6 (1-15) from US08991628.pep 109 1 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 26.619; Variance 37.654; scale 0.707

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DВ	ID	Description	Pred. No.	
, ,	109	100.0	666	<u>ب</u> ا	ілнисз	desmoglein 3 precurso	6.01e-11	
N	65		431	N	S25196	ial		
ω	61	56.0	980	N	T00045	ש		
4	60	55.0	282	N	S43577	C28A5.4 protein (clon	:-	
ر ن	60	55.0	334	μ	G8BPT4	e protei		
σ'n	60	55.0	973	Ν	T01862			
7	59	54.1	163	N	B70854		3.15e+00	
œ	59	54.1	330	N	C71180	Ω		
9	59		360	N	888098	ferric exochelin bios	3.15e+00	
10	59		531	N	C70333	hypothetical protein	3.15e+00	
11	58		332	N	E69312	nitrate reductase gam	4.77e+00	
12	58		469	N	F69075	nitrogenase (EC 1.18.	4.77e+00	
7,1	58	53.2	770	N	PN0105	RNA-directed RNA poly	4.77e+00	
14	58		1237	-	GNFF42	retrovirus-related po	4.77e+00	
15	57		175	N	S48546		7.17e+00	
16	57		387	N	150703	transcription factor	7.17e+00	
17	57		772	N	T02805	chloride channel prot	7.17e+00	
18	57		1013	N	JC2314	chitin synthase (EC 2	7.17e+00	
19	56		212	N	PQ0467	gamma A protein - Poa	1.07e+01	
20	56		360	N	S31264	isocitrate dehydrogen	1.07e+01	
21	56	51.4	482	ν	S31478	alpha-amylase (EC 3.2	1.07e+01	
22	56	51.4	848	4	A44282	retrovirus-related po	1.07e+01	
23	56	51.4	1186	Ν	S70430	hypothetical protein	1.07e+01	

Best Local Similarity 100.0%; Pred. No. 6.01e-11; Matches 15; Conservative 0; Mismatches 0;

Indels

0; Gaps

0;

4.5	44	43	42	41	40	39	3 8	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24
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49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	50.5	50.5	50.5	50.5	51.4	51.4	51.4
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A43426	GNMVGV	GNMVRV	GNVWK	S44792	A42743	S36856	S12588	A69206	A26621	E64383	WMBV2P	S60769	A05069	I49645	S33033	I49149	149279	A56726	S38480	S63985	AD4831
collagen alpha 2 fibr	pol polyprotein - AKV	pol polyprotein – rad	pol polyprotein - AKR	F09G8.8 protein - Cae	pol polyprotein – rad	glycolipid 2-alpha-ma	pol polyprotein - min	hypothetical protein	retrovirus-related en	translation initiatio	29K protein - tobacco	DNA repair/recombinat	pol polyprotein - Rau	polymerase polyprotei	hypothetical protein	CRF receptor - mouse	sauvagine/corticotrop	corticoliberin recept	nonstructural protein	collagen alpha 2 chai	nucrear pore comprex
2.37e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	2.37e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.07e+01	1.07e+01	T.U/e+UI							

ALIGNMENTS

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	SUMMARY
g_site carbohydrate (Asn)	110,180,545
desmoglein repeat #label	937-966
desmodlein repeat #label DG1\	856-016
intrace in ar #status predicted #labe	640-000
	515-53G
cadherin repeat homology #label	106-500
cadherin repeat	270-383
cadherin repeat homology #label	160-267
cadherin repeat homology #label	52-157
edicted	50-615
Ğ	50-999
	24-49
#domain signal sequence #status predicted #label SIG\	1-23
	FEATURE
transmembrane protein	2 EL HONDO
*Superiamity causetts; causetts	CHASSIFICATION
18q12.1-18q12.2	#map_position
m	##cross-
GDB: DSG3	#gene
	GENETICS
	##cross-
AMA	##residues
##molecule type mRNA	
A41088	#accession
pemphigus vulgaris, a disease of cell adhesion. #cross-references MUID:92069753	#cross-refe
ct Ct	#title
	#journal
Amagai, M.; Klaus-Kovtun, V.; Stanley, J.R.	#authors
A41088	REFERENCE
18-Sep-1998 A41088	ACCESSIONS
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change	DATE
desmoglein 3 precursor - numan	TITLE ALTERNATE NAMES
IJHUG3 #type complete	ENTRY
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TITLE
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                        #journal #title
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#accession S25196
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                                                                           #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL:Z46881; NID:g599967; PID:g599977; MIPS:YIL022w
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82-89;112-122;221-228;295-306;316-327;356-370 ##label
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Similarity 57.1%;
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Protein import into yeast mitochondria: the inner membrane import site protein ISP45 is the MPII gene product. $35357
                                                                                                                                                                                                                                                                                                                                                                                                                membrane protein; mitochondrion
#length 431 #molecular-weight 48854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skelton, J.; Churcher, C. submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maarse, A.C.; Blom, J.; Grivell, L.A.; Meijer, EMBO J. (1992) 11:3619-3628 MPII, an essential gene encoding a mitochondri protein, is possibly involved in protein imp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Saccharomyces cerevisiae) protein YI3299.09; protein YIL022w
                Kawaguchi, T.; Ikeuchi, Y.; Tsutsumi, N.; Kan, A.; (
J.; Arai, M.
J. Farment. Bloeng. (1998) 85:144-149
Cloning, nucleotide sequence, and expression of the
                                                                                                                                           cellodextrin phosphorylase - Clostridium thermocellum #formal_name Clostridium thermocellum 22-dan-1999 #sequence_revision 22-Jan-1999 #text_chan
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12-Dec-1997
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schatz, G.
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                                                                                       cross-references MUID: 90384864
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               authors
                    ##cross-references EMBL:X15907; NID:g15321; PID:g15324
##cross-references EMBL:X15907; NID:g15321; PID:g15324
                                                                                                                                                                                                                                                                                                                              224 PPMTLNEQYASPYLY 238
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##molecule_type DNA
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##experimental_source ATCC 27405
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                                                                                                                                                                                                                                                                                                                                                                        55.0%;
Similarity 40.0%;
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#length 980
                                                                                                  Efimov, V.P.; Prilipo
Nucleic Acids Res. (1
Nucleotide sequences
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larity 60.0%;
Conservative
 submitted
                                                                                                                                                                         host Escherichia coli
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77/1; 120/2; 145/3; 225/3 #superfamily unassigned homeobox proteins; homeobox homology
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            Mesyanzhinov, V.V.
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th 282 #molecular-weight 31234 #checksum
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to JIPID, December 1989
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Pred. No. 2.07e+00;
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Pred. No. 1.36e+00;
2; Mismatches 3;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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##cross-references EMBL:AF077408; NID:g3319359; PID:g3319363
##experimental_source cultivar Columbia
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The order of association in the morphogenesis pathway is strictly determined except for gp 11 which can be added at any stage of the pathway. Gp 8 associates to the precursor structure after gp 7 binding and before gp 6 binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene 8 is directed clockwise in the T4 map;
gene 8 overlaps with the 3'-end of gene 7
*superfamily phage T4 baseplate protein gp8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harmon, G.; Langston, Y.; Stoneking, T.; Drone, submitted to the EMBL Data Library, July 1998 The sequence of Arabidopsis thaliana T7M24. T01862
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85.20-86.20
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larity 60.0%;
Conservative
Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barrill, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
                                                                                                                                                           #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998
17-Jul-1998
                                                                                                                                                                                                                  B70854 #type complete
hypothetical protein Rv2991 - Mycobacterium
(strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length: 973 #molecular-weight 112369
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T7M24.4
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hypothetical protein T7M24.4 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouss
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Pred. No. 2.07e+00
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Pred. No. 2.07e+00;
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                                                           ; Gas, S.; Barry
D.; Brown, D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal
#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors
                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
##residues 1-163 ##label COL
##cross-references GB:AL021287; GB:AL123456; NID:g3261508;
##00055-references GB:AL021288
PID:g2791588
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                                                                                                                                                                                                                                                                                             ##molecule_type DNA
##residues 1-330 ##label KAW
##cross-references GB:AP000007; NID:g3236134; PID:d1031777; PID:g3258151
                                                                                                                                                                                                                                ##experimental_source strain OT3
##note this accession replaces an interim accession for a
sequence replaced by GenBank
                                       50 RGLNLRFTSDYNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 NRYTGPYT 14
3 RTLNNRYTGPYTF 15
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Similarity 53.8%;
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Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Ohiku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
DNA Res. (1998) 5:55-76
Complete sequence and gene organization of the genome of a
hyper-thermophilic archaebacterium, Pyrococcus horikoshii
O73.
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Taylor, K.; Whitehead, S.;
Nature (1998) 393:537-544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable N-acetyl-gamma-glutamyl-phosphate reductase -
Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
14-Aug-1998
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#length 163 #molecular-weight 18204
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translation not shown
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87.5%;
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Pred. No. 3.15e+00;
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Pred. No. 3.
                                                                                                         .15e+00
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Best Local
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Best Local
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#title
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*cross-references MUID:95191405
                                                                                                                                                             #gene
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                                                                                                                                                                                                                                                                                                      #title The complete genome of the hyperthermophilic bacterium
Aquifex aeolicus.
#cross-references MuID:98196666
#accession C70333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-360 ##label FIS 1-360 ##label FIS 1-360 ##label FIS
                                                                                                                                                                                                              ##residues 1-531 ##label AQF
##cross-references GB:AE000686; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 RALSDPYPNAYTY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
                                                                                                                                                                                                                                                ##molecule_type DNA
                                                                                                                                                                                           ##experimental_source strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 54.1%;
Local Similarity 38.5%;
                                   80 TLKNRLENPYTF 91
                                                                                  Match 54.18;
Local Similarity 66.78;
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TLNNRYTGPYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily methionyl-tRNA formyltransferase;
phosphoribosylglycinamide formyltransferase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    860888
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Mol. Microbiol. (1994) 14:557-569
Identification of genes involved in the sequestration of iron
in mycobacteria: the ferric exochelin biosynthetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aq_372
#length 531 #molecular-weight 62830
                                                                                                                                                                                                                                                                                                                                                                          Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short
J.M.; Olson, G.J.; Swanson, R.V.
Nature (1998) 392:353-358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C70333 #type complete
hypothetical protein aq_372 - Aquifex aeolicus
#formal_name Aquifex aeolicus
08_May-1998 #sequence_revision 08-May-1998 #text_change
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                                                                       Conservative
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                                                                                                                                                                                                                                                                 preliminary; nucleic acid sequence translation not shown
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homology #label PRGF
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exochelin biosynthesis protein fxbA - Mycobacterium
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Pred. No. 3.15e+00;
5; Mismatches 3
                                                                                      Score 59; I
Pred. No. 3

    Mismatches

                                                                                                                                                                                                            NID:g2983038; PID:g2983043; GB:AE000657
                                                                                                     DB 2;
                                                                                      15e+00
                                                                                                     Length 531;
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RESULT

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Lee, N.H.; Sutton, G.G.; Fleischmann, R.D.; Quackenbush, J.;
Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.;
Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman,
J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs,
T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.;
D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.;
Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese,
C.R.; Venter, J.C.
C.R.; Venter, J.C.
Sulfate-reducing archaeon Archaeoglobus fulgidus.
#cross-references MUID:98049343
#accession E69312
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Best Local Similarity 50.0%;
                                                                                                                                                                   #title Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis and comparative genomics.
#cross-references MUID:98037514
#accession F69075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
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##residues 1-32 ##label KLE
##cross-references GB:AE001069; GB:AE000782; NID:g2689392; PID:g2650124;
                                                                                                                                     ##status
##cross-references GB:AE000916; GB:AE000666; NID:g2622674; PID:g2622685
##experimental_source strain Delta H
                                                                             ##molecule_type_DNA
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                                                                                                                                                                                                                                                                                                                                                              Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.;
Dubols, J.; Aldredge, T.; Bashizzadeh, R.; Blakely, D.;
Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P.;
Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire, R.;
Wang, Y.; Wierzbowski, J.; Gibson, R.; Javani, N.; Caruso,
A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.;
McDougall, S.; Shimer, G.; Goyal, A.; Pietrokovski, S.;
Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
                                                                                                                                                                                                                                                                                                              J.; Reeve, J.N.
J. Bacteriol. (1997) 179:7135-7155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F69075 #type complete
nitrogenase (EC 1.18.5.1) molybdenum-iron protein alpha
- Methanobacterium thermoautotrophicum (strain Delta
#formal_name Methanobacterium thermoautotrophicum
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.
Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graha
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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translation not shown
                                                                                                                                           preliminary; nucleic acid sequence
                                                        1-469 ##label MTH
                                                                                                                translation not shown
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Pred. No. 4.77e+00;
4; Mismatches 2;
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#map_position:
KEYWORDS
FEATURE
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122-239
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Best Local Similarity
Matches 6; Conser
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Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                             720
                                                                                                                                                                                                                                                                                                                                                                                                               ##experimental_source strain 7-2
                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type genomic RNA
##residues 1-118,'FH',125-770 ##label KO4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##experimental_source strain cession PN0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type genomic RNA
##residues 1-118,120-770 ##label
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##residues 1-770 ##label
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#residues 122-770 ##label KO2
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W
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                                                                                                         RTLNNRYTGPYT 14
                                                                                                                                                                                                                                                                                                                                                                           the duplication in this protein results from a tandem duplication in the virus genome found in some, but not all, virus strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PN0107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PN0102
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RNA-directed RNA polymerase (EC 2.7.7.48) 85K
barley stripe mosaic virus (strain 4-2)
strain 12-2; strain 7-2
#formal_name barley stripe mosaic virus, BSMV
30-Sep-1993 #sequence_revision 30-Sep-1993 #td
                                                                                                                                                                                                                                                                                                                       segment 3(II)
duplication; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kozlov, Y.V.; Afanasiev, B.N.; Rupasov, V.V.; Golova, Y.I. Kulaeva, O.I.; Dolja, V.V.; Atabekov, J.G.; Bayev, A.A Mol. Biol. (Mosk.) (1989) 23:1080-1090
The complete nucleotide sequence of barley stripe mosaic virus RNA 3 and its variability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain nitrogenase vanadium-iron protein alpha chain
homology #label VIA
#length 469 #molecular-weight 52866 #checksum 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #superfamily dinitrogenase alpha chain; nitrogenase
  vanadium-iron protein alpha chain homology
  oxidoreductase
GNFF42 #type complete
retrovirus-related pol polyprotein -
melanogaster) retrotransposon 412
                                     GNFF42
                                                                                                                                                                          53.2%;
larity 50.0%;
Conservative
                                                                                                                                                                                                                                                 #region #length 770
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                                                                                                                                                                                                                                                                                                                       nucleotidyltransferase
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                                                                                                                                                                          Score 58; DB 2; I
Pred. No. 4.77e+00;
4; Mismatches 2
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Pred. No. 4.77e+00;
2; Mismatches 3
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Bayev, A.A.
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##molecule_type DNA
1-1;
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#cross-references MUID:86274717
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##cross-references GB:X04132; GB:X03733; NID:g8500;
PID:g1335652
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S48545
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#formal_name Saccharomyces cerevisiae
02-Dec-1994 #sequence_revision 02-Dec-
12-Dec-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily pol polyprotein
aspartic proteinase; hydrolase;
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#active_site Asp (shared with dimeric partner) #st
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:es EMBL:U14913; NID:g544497; PID:g544509; MIPS:YLR193c
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Pred. No. 7.17e+00;
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Search completed: Fri_Jun 11
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MPsrch_pp protein · protein database search, using Smith-Waterman algorithm

Tabular output Run on: not generated Fri Jun 11 17:45:15 1999; MasPar time 2.45 Seconds 173.166 Million cell updates/sec

Title:

Description: Perfect Score: 109 >US-08-991-628-6 (1-15) from US08991628.pep

Sequence: 1 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 27.195; Variance 33.825; scale 0.804

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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29 KD PROTEIN.	DNA REPAIR PROTEIN REC	PROTEIN A43.	29 KD PROTEIN (FRAGMEN	RETROVIRUS-RELATED POL	PROBABLE SERINE/THREON	ZINC CARBOXYPEPTIDASE	CORTICOTROPIN RELEASIN	TRANSCRIPTION FACTOR X	HYPOTHETICAL 28.3 KD P	GVPF/L PROTEIN.	NUCLEOPORIN NUP145 (NU	ISOCITRATE DEHYDROGENA	CHITIN SYNTHASE 2 (EC	TRANSCRIPTION FACTOR G	RETROVIRUS-RELATED POL	NITROGENASE MOLYBDENUM	ZINC CARBOXYPEPTIDASE	BASEPLATE STRUCTURAL P	PUTATIVE HOMEOBOX PROT	TRANSCRIPTION FACTOR X	MITOCHONDRIAL IMPORT I	DESMOGLEIN 3 PRECURSOR	Description	
	8.85e+00		8.85e+00	8.85e+00	5.72e+00	5.72e+00	5.72e+00		5.72e+00	5.72e+00	3.68e+00	3.68e+00	2.35e+00	2.35e+00	1.49e+00	1.49e+00	9.43e-01	5.92e-01	5.92e-01	2.30e-01	5.37e-02	8.99e-13	Pred. No.	

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RRPL_PI2HT	RRPL_MUMPM	C6B2_HELAM	FLHP_BACSU	NUC1_CUNEE	YMCC_EMENI	Y85A_METJA	POL_MLVF5	POL_MLVFF	POL_MLVFP	POL_MLVMO	POL_MLVAV	POL_MLVRD	POL_MLVAK	YLS8_CAEEL	POL_MLVRK	YUR1_YEAST	POL3_MOUSE	GPRA_RAT	Y669_METJA	GAL7_YEAST	POL_MLVCB
RNA POLYMERASE BETA SU	RNA POLYMERASE BETA SU	CYTOCHROME P450 6B2 (E	FLAGELLAR HOOK-BASAL B	NUCLEASE C1 (EC 3.1.30	HYPOTHETICAL 25.4 KD P	HYPOTHETICAL PROTEIN M	POL POLYPROTEIN [CONTA	POLYPROTEIN [POL POLYPROTEIN [CONTA	HYPOTHETICAL 83.6 KD P	POL POLYPROTEIN [CONTA	PROBABLE MANNOSYLTRANS	RETROVIRUS-RELATED POL	PROBABLE G PROTEIN-COU	PUTATIVE ATP-DEPENDENT	GALACTOSE-1-PHOSPHATE	POL POLYPROTEIN (CONTA				
1.36e+01	8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00	8.85e+00			8.85e+00	8.85e+00	8.85e+00	8.850+00						

ALIGNMENTS

DR DR	8888888	8888888888	282222222222222222222222222222222222222	RESULT DD ACC PROCESS OF THE CONTRACT OF THE C
EMBL; M76482; G190752; PIR; A41088; IJHUG3. MIM; 169615; PROSITE; PS00232; CADHERIN; 3. PFAM; PF00028; cadherin; 4. HSSP; P09803; 1EDH.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).	- IOMAIN: CALCIDM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS (POTENTIAL) DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3 SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.	V., STANLEY J.R.; a novel epithelial cadherin in cell adhesion."; OF INTERCELLULAR DESMOSOME JUN DESACTION OF PLAQUE PROTEINS AND CELL-CELL ADHESION. N: TYPE I MEMBRANE PROTEIN. PPIDERMIS, TONGUE, TONSIL, OES	DSG3_HUMAN STANDARD; PRT; 999 AA. DSG3_HUMAN STANDARD; PRT; 999 AA. P32926; 01-OCT-1993 (REL. 27, CREATED) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DESMOCLEIN 3 PRECURSOR (130 KD PENPHIGUS VULGARIS ANTIGEN) (PVA). DSG3. DSG3. BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

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Query Match
Best Local S
Matches 1
                                                                                                                                    SEQUENCE FAVOR ..... STRAIM-SERGE FACTOR AND SERVIN D., BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D., BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D., BARRELL B.G., BADCOCK K., COPSEY T., DEAR S., DEVLIN K., FRASER GENTLES S., HAMLIN N., MONIEL T.S., HUNT S., JAGELS K., JONES LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D., RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V., WALSH S.V., WHITEHEAD S.;
WALSH S.V., WHITEHEAD S.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
MEDLINE; 9345448.

MEDLINE; 9345448.

MEDLINE; 9345448.

HORST M., JENOE P., KRONIDOU N.G., BOLLIGER L., OPPLIGER C., CHATZ G.;

Protein import into yeast mitochondria: the inner membra site protein import into yeast mitochondria: the inner membra site protein ISP45 is the MFII gene product.";

EMBO J. 12:3035-3041(1993).

-I- FUNCTION: INVOLVED IN PROTEIN IMPORT INTO THE MITOCH( PROBABLY INVOLVED IN TRANSLOCATION ACROSS THE INNER! AS A BINDING PROTEIN REQUIRED FOR DRIVING THE IMPORT AS A BINDING PROTEIN REQUIRED FOR DRIVING THE IMPORT AS A BINDING RECRUITS MITOCHONDRIAL HSP70 AND ITS CO
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01-JUL-1993 (REL. 2
01-NOV-1997 (REL. 3
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01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE
PRECURSOR (MITOCHONDRIAL PROTEIN IMPORT PROTEIN
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PROPEP
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"MPII, an essential gene encoding a mitochondrial
is possibly involved in protein import into yeast
EMBO J. 11:3619-3628(1992).
                                                                                                                                                                                                                                                                                                               MAARSE A.C., BLOM J.,
                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; FUNGI; A SACCHAROMYCETACEAE;
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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA, FUNGI, ASCOMYCOTA, HEMIASCOMYCET
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dria: the inner membrane
product.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCASE SUBUNIT TIM44
ROTEIN 1) (INNER MEMBRANE
IMPORT MACHINERY PROTEIN
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       E MITOCHONDRION.
E INNER MEMBRANE.
E IMPORT OF
ITS CO-CHAPERONE
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mitochondria.";
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       CO-CHAPERONE
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       NUCLEAR PROTEIN
                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                          MESOBATRACHIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                      SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: TO OTHER GATA-TYPE TRANSCRIPTION FACTORS
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EMBL; 246881; G599977; -.
EMBL; X67276; G3967; -.
EMBL; Z47047; G763324; -.
PIR; S25196; S25196.
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                               European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffied and this statement is not removed. Usage by and for commercial itles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      (MGE1) TO DRIVE PROTEIN TRANSLOCATION INTO THE MATR AS AN ENERGY SOURCE.
SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT COLLERST 3 DIFFERENT PROTEINS (TIM17, TIM23, TIM44).
SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO DRIVE PROTEIN TRANSLOCATION INTO THE MATRIX
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MBL outstation -
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SGD; L0001138; MPI1.
witochondrion; inner membrane; transport; pro
iranslocation; transit peptide; atp-binding. 13 SSRTLTARYRSQYT Local Similarity 101 431 AA; 59.6%; larity 57.1%; Conservative 431 108 26 48854 WW; Score Pred. MITOCHONDRION.
MITOCHONDRIAL IMPORT TRANSLOCASE SUBUNIT TANSLOCASE SUBUNIT TO ATP (POTENTIAL) 002E0771 re 65; DB 1; Le 1. No. 5.37e-02; Mismatches 4; CRC32 PROTEIN Length 431; INNER MEMBRANE TRANSPORT; Indels 0, Gaps

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SARTLNNRYTGPYT

15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR XGATA-6B (GATA BINDING FACATA-6A OR GATA-6.
XENDERG TATA-6. TISSUE-LIVER;
GOVE C.D., WALMSLEY M., NIJJAR S., BERTWISTLE D., GUI:
GOVE C.D., WALMSLEY M., PATIENT R.;
PARTINGTON G., BOMFORD A., PATIENT R.;
SUBMLITED (CCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: ASSOCIATED WITH CARDIAC SPECIFICATION A
CARDIAC-SPECIFIC TRANSCRIPTION DURING EMBRYOGENES
THE EXPRESSION OF CARDIAC MHC-ALPHA IN VIVO. EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; 15-JUL-1998 (REL. 15-JUL-1998 (REL. 15-JUL-1998 (REL. N.A. PIPOIDEA; STANDARD; PIPIDAE; PRT; XENOPODINAE; 391 AA EMBRYOGENESIS. IFICATION AND FACTOR-6B). XENOPUS GUILLE BATRACHIA; CAN REGULATE 3 ACTIVATES ANURA

EMBL; Y08865; E275165; -.
PROSITE; PS00344; GATA_ZN_FINGER;
PFAM; PF00320; GATA; 2.
HSSP; P17678; 1CAU.
TRANSCRIPTION REGULATION; ACTIVATO modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch). the European Bioinformatics Institute. SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL non-profit institutions as long REGULATION; ACTIVATOR; DNA-BINDING; There are no rest http://www.isb-sib Usage ZINC-FINGER ğ restrictions collaboration ch/announce/ 8 8 its way cial

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Matches 8; Conser
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Best Local :
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P19062;
01-NOV-1990
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SEQUENCE
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PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaborative between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (APR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE DISTAL-LESS FAMILY OF HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEN
RHABDITINA; RHABDITOIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
PUTATIVE HOMEOBOX PROTEIN C28A5.4.
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Q18273;
BACTERIOPHAGE T4.
VIRUSES; DSDNA VIRUSES,
                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN; HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN DNA_BIND 102 161 HOMEOBOX.
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                                                BASEPLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
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nes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
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larity 61.5%;
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OIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
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PROTEIN GP8.
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GATA-TYPE.
POLY-SER.
POLY-THR.
POLY-SER.
POLY-SER.
221DD428 CRC32;
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Pred. No. 2.30e-01
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STAGE;
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 PHAGES; MYOVIRIDAE;
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MBL outstation -
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                                                HYDROLASE;
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Query Match
Best Local Similarity
Matches 6; Conser
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P42788;
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"Nucleotide sequences of bacteriophage T4 genes 6, 7
NUCLEIC ACIDS RES. 18:5313-5313(1990).
- I- FUNCTION: STRUCTURAL COMPONENT OF THE BASEPLATE.
                                                                                 use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMULIUM VITTATUM (BLACK FLY) EUKARYOTA; METAZOA; ARTHROPOL
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
ZINC CARBOXYDEPTIDASE (EC 3.4.17.-) (FRAGMENT).
PROSITE; PS00132; CARBOXYPEPT_ZN_1; PROSITE; PS00133; CARBOXYPEPT_ZN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 94093864.
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                                           L08481;
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ilarity 60.0%;
Conservative
                                              G161186;
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NEMATOCERA;
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Pred. No. 5.92e-01
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RA ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
RA MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI J., REEVE J.N.;
RT GCOMPLET G., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RT GCOMPLET G., RECT IN STRONG COMPACT IN NITROGEN FIXATION ARE
C. -1- FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE
C. -1- FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE
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C. -1- FUNCTION: THE KEY ENZYMATIC REACTION FROTEIN.
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C. -1- CATALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + 6 H(+) + N ORTHOPHOSPHATE.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + 6 H(+) + N ORTHOPHOSPHATE.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + 0 NOTHOPHOSPHATE.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + 0 NOTHOPHOSPHATE.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + N ADP + N ORTHOPHOSPHATE.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + N ADP + N ORTHOPHOSPHATE.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + 0 NOTHOPHOSPHATE.
C. -1- CONTALYTIC AND INORGANIC SULFUR.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + N ADP + N ORTHOPHOSPHATE.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + N ADP + N ORTHOPHOSPHATE.
C. -1- CONTALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + N ADP + N ORTHOPHOSPHATE.
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027605;
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ARCHAEA; EURYARCHAEOTA; METHANOBACTERIACEAE;
                                                                                                                                                                                       SEQUENCE 469
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SMITH D.R., DOUCETTE-STAMM L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-DELTA H
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN
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                                                                                                                                                                                    NITROGEN FIXATION; MOLYBDENUM; IRON-SULFUR AA; 52866 MW; 08177BD4 CRC32;
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I. No. 9.43e-01;
Mismatches 5
                                                             No. 1.49e+00;
Mismatches 3;
                                                                                          No.;
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Best Local s
Matches
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01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
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POSOPHILA MELANOGASTER (FRUIT FLY).

EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA;

PTERYGOTA; DIFTERA; BRACHYCERA; MUSCOMORPHI
BURCH J.B.E., EVANS T.; "GATA-4/5/6, a subfamily of three transcription factors transcribed in developing heart and gut."; J. BIOL. CHEM. 269:23177-23184(1994).
                                                                                                                                                                                                                                                                                                                        GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1193
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PIR; D29349; GNFF42.
FLYBASE; FB90000006; 412.
PROSITE; PS00141; ASP_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EUR. J. BIOCHEM. 158:403-410(1986).
-I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U22.
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01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON 412 [CONTAINS:
PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49);
                                                                                                                                          MEDLINE; 94365018.

LAVERRIERE A.C., MACNEILL C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAT6_CHICK P43693;
                                                                                                                                                                                                                    STRAIN-WHITE LEGHORN;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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"Nucleotide sequence characterization retrotransposon, 412.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POL4_DROME P10394;
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YUKI S., INOUYE S.,
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Similarity 42.9%;
6; Conservative
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Pred. No.
5; Misma
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A; EPHYDROIDEA;
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Best Local Similarity
Matches 6; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHS2_EMENI
P30584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CHITIN SYNTHASE 2 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U11889; G511484; -.
PROSITE; PS00344; GATA_ZN_FINGER;
                                             modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                         PROC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      BOWEN A.R., CHEN-WU J.L., MOMANY M., YOUNG ROBBINS P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FGSC 89;
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                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: PLASMA MEMBRANE-BOUND.
-1- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                    "Classification of fungal chitin synthases.",
PROC. NATL. ACAD. SCI. U.S.A. 89:519-533(1992).
-i- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGE-
-i- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMERICELLA NIDULANS
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TISSUE SPECIFICITY: MORE ABUNDANT IN STOMACH, AND IN SMALL INTESTINE. LOWER LEVELS IN LUNG, LIVER, OVARY AND HEART.
                                                                                                                                                                                                                                                                                         GLUCOSAMINYL) ] (N+1)
                                                                                                                                                                                                                                                                                                                BETA-D-GLUCOSAMINYL)](N) = UDP
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240
387
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larity 46.2%;
Conservative
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ASCOMYCOTA; EUASCOMYCETES;
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259
244
40249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 1; 1
Pred. No. 2.35e+00;
3; Mismatches 4
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POLY-THR.
6E67EA1C CRC32;
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                                                                   http://www.isb-sib
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Best Local
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P28834;
01-DEC-1992
01-JUL-1993
01-NOV-1997
                                                                                                                                                                                                                                                      MEDIINE; 90330530.
MEDIINE; 90330530.
KEYS D.A., MCALISTER-HENN L.;
"Subunit structure, expression, and function of NAD(H)-specific isocitrate dehydrogenase in Saccharomyces cerevisiae.";
I. BACTERIOL. 172:4280-4287(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MULTIGENE
SEQUENCE
                                                                                                                             EMBL; M82939; G168041; -.
PIR; C45188; C45188.
TRANSFERASE; GLYCOSYLTRANSFERASE; TRANSMEMBRANE; CELL WALL;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

DUESTERHOEFT A., FLOETH
HILBERT H., MOESTL D.;
SUBMITTED (MAY-1996) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOCITRATE DEHYDROGENASE (NAD), MITOCHONI (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) IDH1 OR YML037C OR N2690.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                    INCLUDING AMP, NAD+, AND CITRATE.
-!- SUBUNIT: OCTAMER OF TWO NONIDENTICAL SUBUNITS
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
                                                                                                                                                                                                                  GRIVELL L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                            of NAD(+)-dependent isocitrate dehydrogenase cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92355609.
CUPP J.R., MCALISTER-HENN L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., MEDLINE; 92355609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; FUNGI; ASCOMYCOTA; SACCHAROMYCETACEAE; SACCHAROMY
                                                                                                                    -1- ENZYME REGULATION: ALLOSTERICALLY REGULATED
                                                                                                                                                                                                        "Yeast mitochondrial NAD(+)-dependent isocitrate dehydrogenase is
                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                   RNA-BINDING
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 12-27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ARTAESRYPERYSY
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                                                                SIMILARITY: BELONGS TO THE ISOCITRATE DEHYDROGENASES FAMILY.
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                                                                                                                                                                                                                                        94089379
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(REL. 26, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
(NEL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1013 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                            BEDNARZ A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                 FRITZ C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                             VAN OOSTERUM K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEMIASCOMYCETES;
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2.35e+00;
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                                                                           AND ISOPROPYLMALATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       from Saccharomyces
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                                                                                                                      ВХ
                                                                                               IDH1
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is produced through

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SULT 12

D N145_YEAST STANDARD;

C P49687;

C P49687;

DT 01-FEB-1996 (REL. 33, CREATED)

DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE NUCLEOPORIN NUP145 (NUCLEAR PORE PROTEIN NUP145).

GN NUP145 OR YGLO92W.

OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

FUKARYOTA, FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACC'

FUKARYOTA, FUNGI; ASCCHAROMYCES.
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Best Local
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MEDLINE; 94320139.
FABRE E., BOELENS W.C., WIMM
'Nup145p is required for nuc
homopolymeric RNA in vitro v
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 94253246.

WENTE S.R., BLOBEL G.;

WENTE S.R., BLOBEL G.;

"NUP145 encodes a novel yeast glycine-leucine-phenylalanine-glycine

"GLFG) nucleoporin required for nuclear envelope structure.";

J. CELL BIOL. 125:955-969(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE SEQUENCE
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                                                                       between
the Euro
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                                                                                                                                                                                YEAST 13:1077-1090(1997).

-IF FUNCTION: MAY PLAY A DIRECT ROLE IN NUCLEOCYTOPLASMIC -IF FUNCTION ALSO IN PROTEIN IMPORT BINDS HOMOPOLYMERIC ROLE SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX.

-I- DOMAIN: CONTAINS G-L-F-G REPEATS.
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                                                                                                                                                                                                                                                                                                            RIEGER M., BRUECKNER M., "Sequence analysis of 20 chromosome VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C;
MEDLINE; 97435481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
STRAIN-ATCC 26109 / X2180;
MEDLINE; 94253246.
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                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                    SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
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P00351; iOSI.
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                       non-profit institue and this statement
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360
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larity 42.9%;
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or nuclear ex
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Pred. No.
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MITOCHONDRIAL SUBUNIT 1.
BINDING TO ISOCITRATE (BY SIMIL,
7D6BCA76 CRC32;
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Saccharomyces
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A and binds
ed motif.";
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EMBL; Z32672; G496731; -...
EMBL; Z72614; E243975; -...
SGD; L0001294; NUP145.
NUCLEAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               & L are located downstream flos-aquae.";
DNA SEQ. 7:97-106(1997).
-i-FUNCTION: MAY PLAY A SY VESICLE SYNTHESIS.
                                                        Y4ZC_RHISN
P55730;
01-NOV-1997
01-NOV-1997
01-NOV-1997
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KINSMAN R., HAYES
"Genes encoding I
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01-OCT-1996
15-JUL-1998
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CONFLICT
SEQUENCE
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                                    HYPOTHETICAL
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BACTERIA; CYANOBACTERIA;
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Similarity 46.2%;
6; Conservet
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Similarity 53.8%;
7; Conservative
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T 281 282
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R., HAYES P.K.;
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1310
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(REL. 34, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                    (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UP
(REL. 35, LAST ANNOTATION
28.3 KD PROTEIN Y4ZC.
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eam of gvpC i
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Pred.
5; M
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Pred. No. 5.72e+00;
2; Mismatches 4
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NA -> QR (IN REF. 2).
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LMKCTYKI -> FEVYI (IN
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RHIZOBIUM SP.

(STRAIN NGR234).

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Query Match 50.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
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Q91678;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TRANSCRIPTION FACTOR XGATA-6A (GATA BINDING FACTOR-6A).
GATA-6A OR GATA-6.
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000109; G2182749; -. HYPOTHETICAL PROTEIN; PLASMID. SEQUENCE 261 AA; 28349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular basis of symbiosis between Rhizobium and legumes.", NATURE 387:394-401(1997).
-1- SIMILARITY: TO P.SYRINGAE (PV. PHASEOLICOLA) AVIRULENCE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 97305956.
FREIBERG C.A., FELLAY R.,
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BACTERIA; PROTEOBACTERIA;
RHIZOBIACEAE; RHIZOBIUM.
                                                                                                                                                                                                                                                                                                                                                                                            "The Xenopus GATA-4/5/6 genes are associated with cardiac specification and can regulate cardiac-specific transcription during specification and can regulate cardiac-specific transcription during embryogenesis.";
DEV. BIOL. 174:258-270(1996).
-I- FUNCTION: ASSOCIATED WITH CARDIAC SPECIFICATION AND CAN REGULATE CARDIAC-SPECIFIC TRANSCRIPTION DURING EMBRYOGENESIS. ACTIVATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-HEART, AND GUT;
MEDLINE; 96175597.
JIANG Y., EVANS T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERRET X.
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3 RTLNNRYTGP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MESOBATRACHIA; PIPOIDEA;
                                                                                                                                                                                                                                                                             THE EXPRESSION OF CARDIAC MICHAPHA IN VIVO. SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS INTESTINE, AND STOMACH. FOUND AT LOWER LEVEL AND COLON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVRPPH3.
                                                                                                                                                                                                       DEVELOPMENTAL STAGE: EXPRESSED IN CARDIAC PROGENITORS DURING EMBRYOGENESIS AND UPREGULATED DURING GASTRULATION. SIMILARITY: TO OTHER GATA-TYPE TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAIROCH A., BROUGHTON W.J., ROSENTHAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 1; 1
Pred. No. 5.72e+00
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51A967AE CRC32;
                                                                                                                                                                                                                                                                                                     AT HIGH LEVELS IN HEART, AT LOWER LEVELS IN LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
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                                                                                                                                                                                                                                                                                                     PANCREAS
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SQ SQ
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                  B
                                   Query Match 50.5%. Best Local Similarity 53.8%. Matches 7; Conservative
                                                                                    NUCLEAR PROTEIN.

ZN_FING 182

ZN_FING 236

DOMAIN 293
                                                                                                                                 EMBL; U45454; G1209880; -. PROSITE; PS00344; GATA_ZN_FINGER; PFAM; PF00320; GATA; 2. HSSP; P17678; 1GAU.
                                                                           SEQUENCE
                                                                                                                           TRANSCRIPTION REGULATION;
                  120 ARSLNGSYGSHYT 132
 2 ARTLNNRYTGPYT
                                                                         236
293
391 AA;
                                                                                    206
260
298
                                               50.5%;
                                                                           41780
                                                                           XX.
                                                                                                                           ACTIVATOR; DNA-BINDING; ZINC-FINGER;
                                             Score 55; D
Pred. No. 5.
                                                                                    GATA-TYPE.
POLY-SER.
                                      2;
                                                                                                        GATA-TYPE
                                                                           1BC6C528 CRC32;
                                       Mismatches
                                                DB 1; I
5.72e+00;
                                                        Length 391;
                                       Indels
                                       0
                                       Gaps
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Search completed: Fri Jun 11 17:45:23 1999 Job time : 8 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:40:44 1999; MasPar time 6.10 Seconds 134.150 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score: Title: >US-08-991-628-6 (1-15) from US08991628.pep 109 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 26.176; Variance 36.644; scale 0.714

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2798775544321 2798775544321 2798775544321	Result
567 567 568 568 568 568 568 568 568 568	Score
561 5 5 5 6 0 9 5 6 0	Query Match Length
993 1189 980 973 1163 330 330 531 211 211 211 211 211 211 211 211 211 2	
113 120 120 120 120 120 120 120 120 120 120	BB
035902 024780 024780 081508 081508 0053240 0533240 059397 0266695 001124 029749	Ħ
DESMOGLEIN 3 (FRAGMENT POL POLYPROTEIN (FRAGM CELLODEXTRIN PHOSPHORY T7M24 4 PROTEIN. HOSPHORY T7M24 4 PROTEIN ELSO HYPOTHETICAL 18.2 KD P 330AA LONG HYPOTHETICAL 62.8 KD P COAT PROTEIN VP1 (FRAGM NITRATE REDUCTASE, GAM NITRN. CE-FKH-1. HYPOTHETICAL 87.2 KD P ENVELOPE GLYCOPROTEIN SIMILAR TO MSF1 PROTEIN SIMILAR TO MSF1 PROTEIN CODED FOR BY C. ELEGAN CCP. INTEGRASE (FRAGMENT). INTEGRASE (FRAGMENT). ORF DERIVED FROM PROTE	Description
8.75e-01 1.35e+01 1.35e+00 2.09e+00 3.20e+00 3.20e+00 3.20e+00 4.88e+00 4.88e+00 4.88e+00 7.42e+00 7.42e+00 7.42e+00 1.12e+01 1.12e+01 1.12e+01	Pred. No.

54	54 4	54 4	54 4	54 4	54 4	54 4	54 4	54 4		54 4	54 4	54 4	54 4	SS	ភូភ	56	56	56	56	56 5	56 5	56 5	22 56 51	50
.5 4641	.5 1738	.5 1736	.5 1736		.5 1204	.5 1038	.5 857	.5 409	.5 408 14	.5 233	.5 116	.5 105	.5 77	.5 468	.5 380	.4 2115	.4 1823	.4 1099	.4 771	.4 648	.4 482	.4 212	.4 129	. 4
075592	039735	Q83362	092808	P70355	041250	Q83398	Q39392	Q61530	010624	Q83367	Q83376	Q61870	Q96797	074872	082468	Q86500	Q26638	P70248	Q80873	Q80875	Q60051	Q02474	042886	000414
Σ	GAG-POL POLYPROTEIN (P	GAG-POL POLYPROTEIN.	PR180.	GAG-POL POLYPROTEIN.	COMPLETE GENOME (FRAGM	REVERSE TRANSCRIPTASE.	SRK29 PROTEIN KINASE.	INTEGRASE (FRAGMENT).	INTEGRASE (FRAGMENT).	REVERSE TRANSCRIPTASE	REVERSE TRANSCRIPTASE	POL PROTEIN (FRAGMENT)	POL POLYPROTEIN PRECUR	HYPOTHETICAL 52.6 KD P	PROTEIN PHOSPHATASE-2C	M33 RNA FOR A NONSTRUC	2 ALPHA FIBRILLAR COLL	MYOSIN IF.	HYPOTHETICAL 87.3 KD P	HYPOTHETICAL 74.0 KD P	ALPHA-AMYLASE PRECURSO	PUTATIVE RNA-DIRECTED	HYPOTHETICAL 14.9 KD P	ORF DERIVED FROM DI LE
2.52e+01	٠	٠	2.52e+01			2.52e+01				2.52e+01			2.52e+01		1.69e+01	1.12e+01	1.12e+01	1.12e+01	1.12e+01	1.12e+01	1.12e+01	1.12e+01	1.12e+01	1.126+01

ALIGNMENTS

Ser Francos	Qy RESULT	% B O	SO	X D D S	CRE	7 7 7 7 7 7	2888		RESULT
01-NOV-1998 (TREMBLREL. 08, CREATED) 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) POL POLYPROTEIN (FRAGMENT). FUGU RUBRIPES (JĀPANESE PUFFERRISH) (TAKIFUGU RUBRIPES). EUKARYOTA; METAAOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA;	512 SVRTLDRGKYTGPYT 526 : : 1 SARTLN-NRYTGPYT 14 ILT 2 093284 PRELIMINARY; PRT; 1187 AA. 093284:	Query Match 61.5%; Score 67; DB 11; Length 993; Best Local Similarity 66.7%; Pred. No. 9.29e-02; Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;	3 993 AA; 107888 MW; 881794BD CR	□ ₩	ISHIKAWA H., LI K., UITTO J.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKSI- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY). FMBI: HSG016. G230200.	SEQUENCE FROM N.A. STRAIN-BALB/C:	MUS MUSCULUS (MOUSE). MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCUUROGNATHI; MURIDAE; MUSIAE; MUS.	01-JAN-1998 (TREMBLREL. 05, CREATED) 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) DESMOGLEIN 3 (FRAGMENT).	ILT 1 O35902 PRELIMINARY; PRT; 993 AA.

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SON RESULT IN RE
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22 STRAIN-5288C (AB972);

23 MEDLINE; 97313267.

24 JOHNSTON M., HILLIER L., RILES L., ALBERMANN K., ANDRE B., ANSORGE W.,

25 A JOHNSTON M., HILLIER L., RILES L., ALBERMANN K., ANDRE B., ANSORGE W.,

26 A LONIS V., BRUCKNER M., DELIUS H., DUBOIS E., DUSTERHOFT A.,

27 A LOUIS E., FLOETH M., GOFFEAU A., HEBLING U., HEUMANN K.,

28 A HEUSS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,

29 A HEUSS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,

20 A HEUSS-NEITZEL D., HILBERT H., H., MINOSGA T., MOSTL D.,

20 A MULLER-AUER S., NENTWICH U., OBERWALIER B., PIRAVANDI E., POHL T.M.,

20 A PORTETELLE D., PURNELLE B., RECHMANN S., RIEGER M., RINKE M.,

20 A PORTETELLE D., PURNELLE B., SCHOLLER P., SCHWAGER C., SCHWARZ S.,

21 A SCHARFE M., SCHERENS B., SCHOLLER P., SCHWAGER C., SCHWARZ S.,

22 A VIERENDELLS F., VOET M., VOLCKAERT G., VOSS H., WAMBUTT R., WEDLER E.,

23 A VIERENDELS F., VOET M., VOLCKAERT G., TOSS H., WAMBUTT R., WEDLER E.,

24 A VIERENDELS F., VOET M., VOLCKAERT G., HANI J., HOHEISEL J.D.;

25 THE NUCLEOCIDE SEQUENCE OF SACCHAROMYCES CEREVISIAE Chromosome

27 XII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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      Matches
                                       Query Match
Best Local
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Q05776 PRELIMINARY; PRT; 175 AA.
Q05776
01-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
SIMILAR TO MSF1 PROTEIN.
L8167.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 1 from the central African Republic."; AIDS RES. HUM. RETROVIRUSES 9:997-1006(1993). EMBL; L11498; G305527; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94107601.
MURPHY E., KORBER B.T., GEORGES-COURBOT M.C., YOU B., PINTER A., COOK D., KIENY M.P., GEORGES A., MATHIOT C., BARRE-SINOUSSI F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIRARD M.;
                                                                                                                           SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; U14913; G544509; -. SEQUENCE 175 AA; 20108 MW; 9FCA0042 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENVELOPE PROTEIN.
                                                                                                                                                                                                                       STRAIN-S288C (AB972);
CHERRY J.M.;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Diversity of V3 region sequences of human immunodeficiency viruses type 1 from the central African Republic.";
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (SEP-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (SEP-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAULEY
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nes 7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 NTRYTGSYTL 72
| ||||:||:
6 NNRYTGPYTF 15
Match 52.3%;
Local Similarity 46.2%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AA;
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Score 57; DB 3; 1
Pred. No. 7.42e+00;
4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 14;
Pred. No. 7.42e+00;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15E98296 CRC32;
                                                          Length 175;
3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 80;
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19 SRAFFNRYPNPYS 31

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0y 2 ARTLNNRYTGPYT 14
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Search completed: Fri Jun 11 17:42:47 1999 Job time: 123 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Jun 11 17:52:50 1999: MasPar +ime / 77 Schools

Run on: Fri Jun 11 17:52:50 1999; MasPar time 4.77 Seconds
Tabular output not generated. 66.862 Million cell updates/sec

Title: >US-08-991-628-7

Description: (1-15) from US08991628.pep

Perfect Score: 99

Sequence: 1 QSGTMRTRHSTGGTN 15

Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 17.125; Variance 54.917; scale 0.312

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length:	₽B	ΠD	Description	Pred No
-	99	100.0	15	20 :	W04847		
N	99	100.0		o i	R30747	בסיונים של סו	5.56e-04
w	л 2	n i	n (ه د	5000	Human pemphigus vulga	5.56e-04
- (· (0/2	۱ ۲-	K06023	^	5.666+01
1 4	. e	4	140	N	R10423	Nod L gene product	830101
U	4.00	48.5	802	Ξ	R56550		1.000
σ	48	48.5		77	N L E U B M	201111111111111111111111111111111111111	2.296+02
7	40	. 40		3	11000	CTITA (CTASS II CLANS	2.29e+02
30	, <u>,</u>	n (1 907	, ⊢	****	Class II trans activa	2.29e+02
0 (1	1000	6	P61048	A.nidulans phosphenol	2.29e+02
	4	0 0	TIOO	. ~	WR0312	CIITA (class II trans	
		\$0.0	TISU	Ĕ	W57056	Class II trans activa	
1	40	48.5	1130	3	W80313		0 0 0
12	48	48.5	1130 1	4	R73453	1 6	
13	48	4.0	7130	Z :	101100	Crass II Cransactivat	2.29e+02
14	48	Д. Д	1207	1 6	20077		2.29e+02
15	47	47 5		ט נ	100011	CLITA (Class II trans	2.29e+02
5	47	47.5		ŏ	\$ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	Alpha-amylase protein	
	:	;	4	*	NZ3434	Alpha amylase mutant	2.87e+02

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	4/			‡ - L			, .) .) ¢	4 .	4.	4.7	47	47	47	4.7	47	47	4	4 /	4.7	47	4.7	47	4	÷.	; 4	, t	7	47
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ALIGNMENTS	W23603	W22523	W22522	W73509	W05236	W05234	E6T08M	91208W	68108M	R58736	R10576	R58727	R58748	R58747	W05228	W05230	W80194	W57973	W57972	W08203	W08205	R58741	R58745	R57986	523	801	873	101	2	2
	e-CenA c	-amylase-CenA c	-amy	-amy	'n	Bacillus licheniformi	A4 form alpha-amylase	form	form	lpha-amylase.	tant alph	alpha-amvlase	C alpha-amylas	Υ.	icheniform	Bacillus licheniformi	Bacillus licheniformi	Alpha-amylase mutant	Alpha-amylase mutant	cheniformis muta	cheniformis m	alpha-amvlase	alpha-amylas	lase.	llus lichenifo	elpha 🤉	5P alpha-amylas	97Y alpha-amyl	or alpha-amylas	
	2.87e+02	87e+0	87e+0	87e+0	87e+0	87e+0	87e+0	87e+0	87e+0	8	30,	20, 0	œ (30 0	2.876+02	00 0	000	870+0	87e+0	. 87e	870+0	876+0	870+0	870+0	876+0	.87e+0	.87e+0	.87e+	•	

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Matches
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Best Local S
Matches
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Best Local Similarity 100.0%;
Matches 15; Conservative
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US7798918-A.
15-DEC-1992.
27-NOV-1991; 798918.
27-NOV-1991; US-798918.
(USSH) US DEPT HEALTH & HUM
Amagai M, Klaus-Kovtun V,
WPI; 93-067436/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /f 2
R30742 standard;
R30742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RO6023;
04-DEC-1990 (first entry)
Viral haemagglutinin neuraminidase.
Haemagglutinin neuraminidase; vaccin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; SOpp; English. This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-1993 (first entry)
Human pemphigus vulgaris 130kb antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein; cell adhesion.
                                                                                                                                                                                                                                                                                                                                                  Recombinant vaccinia virus - is which all or part of DNA coding membrane fusion protein in combined to genom region. Disclosure; p; Japanese. Fragment of parainfluenza viral membrane fusion protein encoding may be incorporated into the vaccina virus, which may then be use as a live vaccine for cows.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 93-067436/08.
N-PSDB; Q35992.
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09-DEC-1988; JP-311655.
(JAPG ) NIPPON ZEON KK.
WPI; 90-228484/30.
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702156883-A.
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15; Conservative
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Pred. No. 5.56e-04;
                                                                                                                                                                                                              Score
Pred.
4; M
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No. 5.66e+01;
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       RESULT
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W80314 standard; Protein; W80314;
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Query Match
Best Local Similarity
Matches 6; Conser
                                                                           Query Match
Best Local Similarity
Matches 8; Conser
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21-JAN-1993; US-007107.
(UYFL) UNIV FLORIDA.
GUY CL, Haskell DW, HO
WPI; 94-264100/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q10325.

Nod genes and control sequences of Bradyrhizobium japonicum - used for improving nodulation and for prodn. of foreign protein, e.g. plant parasite toxin
pisclosure; Page 4; llpp; English.
The nod I gene product may be used to restore nodulating ability to Nod- mutants of Bradyrhizobium or Rhizobium strains and can enhance nodulating ability.

Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-1987; 077561.
24-JUL-1987; US-077561.
(STACEY G. Schell MG, Nieuwkoop AJ, Deshmane NA, Banfalvi Stacey G. Schell MG, Nieuwkoop AJ, Deshmane NA, Banfalvi WPI; 91-036225/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nod L gene product.
Nod genes; parasite; toxin;
Bradyrhizobium japonicum.
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                                                                                                                                              transformation

Claim 6; Page 29; 49pp; English.

Claim 6; Page 29; 49pp; English.

Transgenic plants expressing this cold acclimatization

Protein have improved cold tolerance and/or drought-resistance.

The cell expressing the protein is from the family Solanaceae,

a citrus plant, a bacterium or a yeast cell.

Sequence 802 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R10423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cold acclimatization protein CAP160 from spinach leaf. Cold acclimatization; cold-tolerance; transgenic plant drought-resistance; drought-tolerance; crop improvemen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JAN-1991
                                                                                                                                                                                                                                                                                                                 Cold accilmatisation proteins CAP85 and CAP160 and their nucleotide sequences - used to confer increased cold tolerance and drought resistance on plants and microorganisms by genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spinacia oleracea.
WO9417186-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R56550;
20-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q70904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                freezing-tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R56550 standard; Protein;
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4 TMRTRHSTGGTN 15
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QSGTMRTRHSTGGTN
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                                                                                48.5%;
larity 53.3%;
Conservative
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Pred. No. 1.82e+02;
5; Mismatches 1
                                                                                Score 48; DB 11;
Pred. No. 2.29e+02;
1; Mismatches 6
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improvement;
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                                                                                                                             Length 802
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ACCOMPANIE PRESENTATION OF THE PRESE
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The present sequence represents type IV CIITA (class II transactivator) protein. The products can be used to treat diseases for which centanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially conterferon-gamma or interleukin-4. Inhibitors of the gene or protein coding for MHC class II molecules is desired for dendritic cells or after induction by a cytokine, especially conterferon-gamma or interleukin-4. Inhibitors of the gene or protein coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                            08-OCT-1997; G02751.
21-MAR-1997; GB-005911.
08-OCT-1996; GB-020940.
(CHIL-) INST CHILD HEALTH.
Fabre JW, Gustafsson KT, Yu
WPI; 98-240813/21.
rejection
Claim 15; Pages 69-72; 104pp; English.
This represents a 151 deletion mutant (CIITA) polypeptide. The N-terminal re
                                                                                           N-PSDB; V28717.

Deleted form of the class II trans-activator that reduces class II antigen expression - and ribozyme directed to trans-activator mRNA, related nucleic acid, vectors, transformed cells and antibodies, used for treating auto-immune disease and to inhibit xeno-graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mach
WPI;
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CIITA (class II transactivator) type IV protein.
CIITA gene; class II transactivator; MHC class I
interferon-gamma; interleukin-4; vaccine; cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class II trans activator (CIITA) 151 deletion mutant. Class II trans activator; MHC; CIITA; autoLimune disease; trestransplantation; xenograft; major histocompatibility complex; gene therapy; arthritis; ribozyme; 151 deletion mutant.
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16-APR-1998.
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22-APR-1997;
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5; Conservative
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FR-004954.
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1. No. 2.29e+02;
Mismatches 0;
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CIITA is
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interferon-gamma;

interleukin-4;

vaccine;

II molecule;
er treatment.

sapiens.

EP-874049-A1.

21-APR-1998; 22-APR-1997; 28-OCT-1998 HOMO

400968. FR-004954.

Mach (TRGE

8

TRANSGENE SA

O1-FEB-1999 (first entry)
CIITA (class II transactivator) type II protein
CIITA gene; class II transactivator; MHC class I

W80312 standard; W80312;

Protein; 1106 AA.

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01-FEB-1999

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Anacystis nidulans.
J61056082-A.
                                                          1054 tglmrsryskg
                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 16pp; Japanese.
Transforming a bacteria with the PPC encoding sequence intensifies CO2 fixation ability. Other PPC genes may also be found by hybridisation with an A.nidulans derived probe.
                                                                                                                                                                                                                                                                                                                                                                                            bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                     PPC gene of cloned photosynthetic microorganisms intensifying photosynthesis carbon di:oxide-fixing
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WPI; 86-115948/18.
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Similarity 54.5%;
6; Conservative
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Similarity 55.6%;
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No. 2.29e+02;
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. No. 2.29e+02;
Mismatches 3;
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This represents a class II trans activator (CITTA) polypeptide. When the N-terminal region of the CITTA is deleted, it can be used for reducing the expression of major histocompatibility complex (MHC) class II antigens. A ribozyme targeted to-bases 1159-1161 (GUA) of human CITTA mRNA, or corresponding target in other species and the CITTA polypeptide can be used to reduce expression of MHC class II antigens, particularly for treatment of autoimmune disease (e.g. arthritis and diabetes) or to treat non-human animals intended as source of xenografts. The ribozyme and the CITTA polypeptide may be generated in vivo by gene therapy, using the encoding nucleic acids targeted for localised suppression of the immune response. Material from transgenic animals in which at least some cells are stably transfected with the CITTA encoding nucleic acids are used for animal-to-human transplantation. The CITTA polypeptide constitutively or after lymphokine induction. It has no transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class II trans activator (CIITA) polypeptide.

Class II trans activator; MHC; CIITA; autoimmune disease; treatment; transplantation; xenograft; major histocompatibility complex; diabetes; gene therapy; arthritis; ribozyme.
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W57056;
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DNA encoding MHC class II trans-activator polypeptide(s) e.g. as primers for enzymatic amplification, as detection as inhibitors of expression of genes encoding MHC in denda claim 10; pages 58-61; 86pp; French.
                                                                                                                                                                                                                                                                            This represents a class II trans
                                                                                                                                                                                                                                                                                                                                          Deleted form of the class II trans-activator that reduces class II antigen expression - and ribozyme directed to trans-activator mRNA, related nucleic acid, vectors, transformed cells and antibodies, used for treating auto-immune disease and to inhibit xeno-graft
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21-MAR-1997; GB-005911.
08-OCT-1996; GB-020940.
(CHIL-) INST CHILD HEALTH.
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16-APR-1998.
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1 QSGTMRTRH 9
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llarity 55.6%;
Conservative
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Pred. No.
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3. 2.29e+02;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PT DNA encoding MHC class II trans-activator polypeptide(s) - useful PT e.g. as primers for enzymatic amplification, as detection probes or PT as inhibitors of expression of genes encoding MHC in dendritic cells Claim 31; Pages 62-66; 86pp; French.

CC The present sequence represents type III CITA (class II transactivator) protein. The products can be used to treat diseases for which cenhanced expression of genes coding for MHC class II molecules is C desired, especially where the enhanced expression is desired in CC dendritic cells or after induction by a cytokine, especially for can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
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class II
Sequence
                                                                                                                                                                                                                                 CIITA gene; class
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W80313 standard;
W80313;
                     binding_site
                                                             region
                                                                                                    region
                                                                                                                                                                                                                                                                                                                                                         R72452;
08-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   r 12
R72452 standard; Protein; 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 98-559115/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1998;
22-APR-1997;
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                                                                                                                                              region
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                                                                                                                                                                                                           Key
                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  797
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1130 AA;
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class II transactivator; MHC class II
amma; interleukin-4; vaccine; cancer t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                      /note- ".
261..322
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                                                                                                                                                  163..195
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                                                                                                                                                                  note-
                                                                                                                                                                                                           Location/Qualifiers
                                         note-
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55.6%;
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                     .426
                                                                                                                                                                    "acidic
                                       "region
                                                                                 "region
                                                                                                                        "region
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Pred. No.
4; Misma
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Pred. No. 2.29e+02;
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                                         III rich
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                                                                                   rich
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2.29e+02;
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                                       in Pro/Ser/Thr"
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For Gene encoding a protein displaying class II trans-activator of gene encoding a protein compsn. for treating diseases associated with impaired expression of MHC-II genes, etc.

Pr with impaired expression of MHC class II genes expression in Bymphocytes. The DNA class II gene expression in Bymphocytes. The DNA cc sequence has two in frame start codons. The first of these is at position In 6 and acts as the translation initiation site. The second is present cc (at position 188) in the context of a perfect Kozak box and may also contains three stretches rich in proline/serine/threonine. It also contains three stretches rich in proline/serine/threonine. It also contains a region rich in glutamate/aspartate (an acidic region) and an CC archains a region rich in glutamate/aspartate (an acidic region) and an CC archains a region rich in glutamate/aspartate (an acidic region) and an CC archains a region rich in glutamate/aspartate (an acidic region) and an CC acids 979 to 1061 that shows weak homology with the N terminal portion of a yeast RNA binding protein. The protein can be used for the CC aguence can be used to treat diseases where a decrease in the level of cartheirs and multiple sclerosis, lupus erythematosis and rheumatoid cartheirs.
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Best Local s
Matches
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(MACH/) MACH B F.
MACH BF;
                                                                                                                                                                        W09606107-A1.
29-FEB-1995, U10691.
22-AUG-1995, U8-295502.
24-AUG-1994; US-295502.
(HARD ) HARVARD COLLEGE.
Douhan J, Glimcher LH,
WPI; 96-151325/15.
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19-APR-1995.
26-AUG-1994;
26-AUG-1993;
Methods which inhibit transcription activation by CIITA - causes inhibition of MHC class II gene expression, used in therapy of auto:immune disorders

Example 1; Page 36-41; 64pp; English.
A genomic DNA sequence (T18028) codes for the class II transactivator, CIITA (R81599), a protein essential for activation of transcription of MHC class II genes. The CIITA transcription activation formation domain provides useful information for identifying cpds which inhibit CIITA-dependent transcription. Such cpds. are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                797 qpgtlrarg 80
|:||:|:|:
1 QSGTMRTRH 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                           N-PSDB; T18028.
                                                                                                                                                                                                                                                                                                                     domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R81569 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                        lass II transactivator.
IITA; class II transactivator; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 48.5%;
Local Similarity 55.6%;
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301..1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                       352
                                                                                                                                                                                                                                                                                                    "interaction domain"
                                                                                                                                                                                                                                                                                                                                     "transcription activation
                                                                                                                                                                                                                                                                                                                                                                                                                          complex class II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48;
Pred. No.
4; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease;
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RESULT PROPERTY OF SECOND PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a type I CIITA (class II transactivator) protein. The products can be used to treat diseases for which enhanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially interferon-gamma or interleukin-4. Inhibitors of the gene or protein can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
                                                      11-FEB-1993;
06-JUN-1995;
(GEMV ) GENEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 98-559115/48.

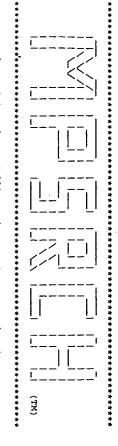
DNA encoding MHC class II trans-activator polypeptide(s) - useful e.g. as primers for enzymatic amplification, as detection probes as inhibitors of expression of genes encoding MHC in dendritic ce as inhibitors of expression of genes encoding MHC in dendritic ce Claim 10; Pages 53-57; 86pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease therapeutics. Sequence 1130 AA;
                                                                                                                                                                                                                                                     Alpha-amylase protein variant M197T. PCR primer; alpha-amylase; variant; oxidative stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIITA (class II transactivator) type I protein.
CIITA gene; class II transactivator; MHC class II molecule;
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W80311 standard; Protein; 1207
       Barnett
Solheim
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EP-874049-A1.
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22-APR-1997;
                                                                                                                                                                                                            US5849549-A.
                                                                                                                                                                                                                                 Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                      02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                             W73510 standard;
W73510;
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                                                                                                                                 10-FEB-1994;
                                                                                                                                                           06-JUN-1995;
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US-468698.
V ) GENENCORTINT.
tt CC, Mitching
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larity 55.6%;
Conservative
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FR-004954.
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55.6%;
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Pred. No. 2.29e+02;
4; M1smatches 0;
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Pred.
4; M
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                                    SD,
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                                 Requadt
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2.29e+02;
0;
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Starch liquefaction - using mutant Bacillus alpha-amylase Disclosure; F19 4a; 56pp; English.
This sequence represents the M197T variant of the Bacillus licheniformis alpha-amylase. Variants of the protein can be used in the method of the invention, for liquefying a granular starch slurry from a wet or dry milling process at a ph of 4 to less than 6, that comprises adding a mutant Bacillus alpha-amylase to the slurry, optionally adding an antioxidant, and reacting the slurry until the starch is liquefied. The alpha-amylase has a substitution of Thy, Leu, Asn or Asp for a Net residue corresponding to M15 in B. licheniformis alpha-amylase. Alternatively the alpha-amylase has a substitution of Leu or Ala for a residue corresponding to M197 in B. licheniformis alpha amylase. Mutants such as M197L and M15L have enhanced oxidative stability at pH 5.
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Gaps ö Score 47; DB 38; Length 483; Pred. No. 2.87e+02; 3; Mismatches 3; Indels Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative

69 qkgtvrtkygtkg 81 | ||:||: :| | | QSGTMRTRHSTGG 13 g ò

Search completed: Fri Jun 11 17:54:36 1999 Job time : 106 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Fri Jun 11 17:57:22 1999; MasPar time 4.34 Seconds 138.367 Million cell updates/sec

Description:
Perfect Score:
Sequence: >US-08-991-628-7 (1-15) from US08991628.pep 99 1 QSGTMRTRHSTGGTN 15

Title:

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 23.847; Variance 29.890; scale 0.798

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2221165433211222222322232222222222222222222222	Result
44445555555555555555555555555555555555	Score
100 570 570 570 571 571 571 571 571 571 571 571 571 571	% Query Match
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IJHUG3 S14666 S31886 A44991 S33568 A44991 FVHUCY TVHUCY TO3369 JN0378 S04605 S04605 S04605 S04605 JE0471 JE04713 HNNZB3 S45306 A25979 A25979 A60712 I49713	ID
desmoglein 3 precurso keratin 10, type I, c sol protein large sp DNA-directed RNA poly protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina gene m3 protein Lac p-Aminobenzoic acid s glycinin G3 - soybean glycinin G3 precursor glycinin chain AlaBx glycinin G1 precursor glycinin G1 precursor glycinin G1 protein moutch 3 protein mourami notch 3 protein mourami notch 3 protein mourami notch 3 protein mourami notch 3 protein mouse H-2K-s mouse H-2K-sm1 - mouse hypothetical protein	Description
1.83e-11 3.92e-01 6.39e-01 1.04e+00 1.04e+00 1.04e+00 1.04e+00 1.04e+00 2.99e+00 6.80e+00 6.80e+00 6.80e+00 6.80e+01 1.07e+01 1.07e+01 1.07e+01 1.07e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01 1.68e+01	Pred No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5
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tensin - chicken (fra	probable membrane pro	toxR-regulated lipopr	alpha-amylase (EC 3.2	nucleocapsid protein	bam protein - fruit f	filaggrin precursor -	probable ribosomal pr	extracellular nucleas	invasion-inducing pro	coatomer complex alph	MHC class II transact	phosphoenolpyruvate c	cell division control	phosphoprotein - fiss	nitrate reductase (EC	protein-serine/threon	hypothetical protein	exo-alpha-sialidase (bindin fertilization	transcription factor	scytalone dehydratase
4.03e+01	4.03e+01	4.03e+01	4.03e+01	4.03e+01	4.03e+01	4.03e+01	4.03e+01	2.61e+01 2.61e+01	2.61e+01	2.61e+01	2.61e+01										

ALIGNMENTS

Query Match Best Local Similarity Matches 15; Conse	SUMMARY	937-966. 937-180,545	510-539 540-539	160-267 270-383 390-495	24-49 50-999 50-615	FEATURE	######################################	#gene	##molecule ##residues ##cross-re	#title #cross-refere #accession	#authors #journal	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM ORGANISM ACCESSIONS
100.0%; Score 99; DB 1; Length 999; nilarity 100.0%; Pred. No. 1.83e-11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#length 999 #molecular-weight 107502 #checksum 8311	#domain desmoglein repeat #label DG2\ #binding_site carbohydrate (Asn) (covalent) #status	transmembrane #status predicted intracellular #status predicted democration proper #label DC1	#comain cacherin repeat homology #label CR2\ #domain cacherin repeat homology #label CR3\ #domain cacherin repeat homology #label CR3\ #domain cacherin repeat homology #label CR4\ #domain cacherin repeat homology #label CR4\	propeptide #status predicted #label PRO\ t desmoglein homolog #status predicted #label EX extracellular #status predicted #label EX	#domain signal sponence #status predicted #label SIGN	rerences GDB:134030; OMIM:169615 18q12.1-18q12.2 #superfamily cadherin; cadherin repeat homology calcium binding; cell adhesion; duplication; glycoprotein; transmembrane protein	GDB:DSG3	H 1	title Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion. cross-references MUID:92069753 accession A41088	Amagai, M.; Klaus-Kovtun, V.; Stanley, J.R. Cell (1991) 67:869-877	IJHUG3 #type complete desmoglein 3 precursor - human pemphigus vulgaris antigen #formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 18-Sep-1998

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                                                                              #accession
                                                                                          structural brain gene *cross-references MUID:91334436
                                                                                                                                                     #journal
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##residues 1-453 ##label DAR1
##cross-references EMBL:M19156
the sequence from Fig. 3 is inconsistent with the
nucleotide sequence from Fig. 2 in having additional
residues ile-Lys-lle-Arg-Leu after 313-Leu
##residues 1-1597 ##label DEL
##cross-references GB:M64084; NID:g2760822; PID:g158483
The sol (small optic lobes) mutation eliminates certain classes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:M19156
.FICATION #superfamily cytoskeletal keratin
.DS coiled coil; heptad repeat; inter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 57.6%; Similarity 50.0%; 7; Conservative
                                                                                                Miklos, G.L.G.
Miklos, G.L.G.
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:7214-7218
Molecular cloning and analysis of small optic lobes
structural brain gene of Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M. submitted to the EMBL Data Library, May 1988 $14669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M. Mol. Biol. Rep. (1987) 12:277-283
Sequence of a cDNA encoding human keratin No 10 selected according to structural homologies of keratins and their tissue-specific expression.
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#formal_name Homo sapiens #common_name man
30-Sep-1991 #sequence_revision 31-Dec-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain tail #status
#length 453 #checksum 131
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$14666
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keratin 10, type I,
                                                                                                                                                                                                                                                                #formal_name Drosophila melanogaster
30.Jun-1992 #text_change
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                                                                                                                                                                                       Delaney, S.J.; Hayward, D.C.; Barleben, F.; Fischbach, K.F.;
                                                                                                                                                                                                              A41146
                                                                                                                                                                                                                                                                                                         melanogaster)
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                                                                                                                                                                                                                                                                                                                           protein,
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#domain helical rod #status predicted #label ROD\
#domain tail #status predicted #label TAI
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                                                                                                                                                                                                                                                                                                                         large splice form -
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Pred. No. 3.92e-01;
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                                                                                                                                                                                                                                                                                                                         fruit fly (Drosophila
                                                                                                                                small optic lobes, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 453;
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673-702
713-730
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                                                                                                                                                                                                                                             ##molecule_type DNA
#residues 1-124 ##label_KA2
                                                                                                                                                                                                                           ##cross-references EMBL:X66452
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                                                                                                                                                                      RPB1
SGC9
                                                                                                            *superfamily human DNA-directed RNA chain
                                                       DNA binding; nucleotidyltransferase; transcription; zinc finger #length 478 #checksum 3090
                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. (1992) 20:5985-5989

Nucleic Acids Res. (1992) 20:5985-5989

TGA cysteine codons and intron sequences in conserved nonconserved positions are found in macronuclear RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S33886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene dosage as a possible major determinant for equal expression levels of genes encoding RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S33886 #type fragment
DNA-directed RNA polymerase (EC
RPB1 - Euplotes octocarinatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily sol protein; calpain catalytic domain homology alternative splicing; brain; zinc finger
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                                                                                                                                                                                                                                                                                                                          polymerase
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#region zinc finger CCCC motif\
#domain calpain catalytic domain homology #label CALP\
#domain calpain catalytic domain homology #label CALP\
#domain telle Cys, His, Asn #status predicted
#active_site Cys, His, Asn #status predicted
#active_site Cys, His, Asn #status predicted
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#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
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 56.6%;
                                                                                                                                                                                                                                                                                                                            genes of Euplotes
 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 1; L
Pred. No. 3.92e-01;
3; Mismatches 2
 56; DB 2; I
No. 6.39e-01;
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##cross-references GB:M2726; NID:g193357; PID:g309241
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protein-tyrosine kinase (EC 2.7.1.112) fyn -
kinase-related transforming protein (fyn)
fformal_name Mus musculus #common_name house
03.Jun-1993 #sequence_revision 30-Sep-1993 #t
08-Sep-1997
                                                                       submitted to S36351
                                                                                                                                                                                                                                                                                 J.; Yamamoto, T.
Oncogene (1993) 8:823-831
A novel Yes-related kinase,
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New Biol. (1989) 1:66-74
Expression of a novel form of the
hematopoietic cells.
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es EMBL:X52841; NID:g62861;
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Similarity 57.1%;
Hannig, G.; Ottilie, S.; Schartl, Oncogene (1991) 6:361-369
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#journal Oncogene (1990) 5:369-376
#title Structure and expression of fyn genes in Xenopus laevis.
#cross-references MUID:90191723
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p59(Xfyn) - Xiphophorus helleri
#formal_name Xiphophorus helleri
04-Sep-1997 #sequence_revision 0
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homology; St2 homology; SH3 homology
ATP; phosphoprotein; phosphotransferase; F
transforming protein; tyrosine-specific
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Matches
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O81508 PRELIMINARY;

O81508;

O1-NOV-1998 (TREMBLREL 08, C
01-NOV-1998 (TREMBLREL 08, L
01-NOV-1998 (TREMBLREL 08, L
77M24.4 PROTEIN.
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024780
024780;
01-JAN-1998
01-JAN-1998
01-AUG-1998
                                                                                                                                                                                                                       T7M24.4.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIFLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;.
                                                                                                          STRAIN-CV. COLUMNIA;
HARMON G., LANGSTON Y., STONEKING T., DRON
Le sequence of Arabidopsis thaliana T7M
MITTED (JUL-1998) TO EMBL/GENBANK/DDBJ

(2)
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"A retrotransposon family from
GENE 215:241:249(1998).
EMBL; AF03C381; G3510505; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAWAGUCHI T., IKEUCHI Y., TSUTSUMI N., FERMENT. BIOEMG. 85:144-149(1998). EMBL; AB00682; D1029240; ... ABBAE3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDP
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                                                          SEQUENCE FROM N.A.
STRAIN-CY. COLUMBIA;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLOSTRIDIUM THERMOCELLUM BACTERIA; FIRMICUTES; BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELLODEXTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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"The Arabidoybis thaliana Genome Sequencing Project.";
SUBMITTED (JÜL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
        SUBMITTED
                                             WASHU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC27405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSTRIDIUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SARTLNNRYTGPYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
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1187
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3 (TREMBLREL. 05,
3 (TREMBLREL. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 2;
Pred. No. 1.35e+00
2; Mismatches
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No. 8.75e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pufferfish
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                                                                                                                                                                                                                                                                                                                                                                                                                                              973
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                                                                                                                                           T7M24.";
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                                                                                                                         BANKS
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Best Local S
Matches
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Best Local
                                                                                                                                                                                                                                                                                  TLT 6
059397
059397;
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STRAIN-H37RV;
OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) T
                                                                                                                                                                               01-AUG-1998
01-AUG-1998
01-JAN-1999
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053240
053240;
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STRAIN-CV. COLUMBIA;

WATERSTON R.;

WATERSTON R.;

SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

SEMBL; AF077408; G3319363; -

SEQUENCE 973 AA; 112369 MW; F6086EE2 CRC32;
   ARCHAEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIACEAEE; MYCOBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIACEAEE; MYCOBACTERIACEAEEE
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01-JUN-1998 (TREMBLREL 06, I
01-NOV-1998 (TREMBLREL 08, I
HYPOTHETICAL 18.2 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROC. NATL. ACAD. SCI. U.S.A. EMBL; AL021287; E1237736; -.
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SUBMITTED (JA)
                                                                        PYROCOCCUS
                                                                                                                                            330AA LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BALASUBRAMANIAN V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96181548.
PHILIPP W.J., POUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-H37RV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ERYTGPYT 118
:||||||
7 NRYTGPYT 14
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Similarity 53.8%;
7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 54.1%;
Similarity 87.5%;
7; Conservative
                                  EURYARCHAEOTA;
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                                                                                                                                                                           GIREMBLREL.
GIREMBLREL.
GIREMBLREL.
                                                                        HORIKOSHII.
                                                                                                                                            HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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AN V., HEYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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                                                                                                                             07, CREATED)
07, LAST SEQUENCE UPDATE)
09, LAST ANNOTATION UPDATE)
N-ACETYL-GAMMA-GLUTAMYL-PHOSDHATE
                                  THERMOCOCCALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.A., PARKHILL J., COLE S.T. EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GENBANK/DDBJ DATA BANKS
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B., BERGH
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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2.09e+00;
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BLOOM B.R., JACOBS
                                  THERMOCOCCACEAE;
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Best Local
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Q50378;
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                                                                                                                                                                                                                                                                                                                                                      "Identification of mycobacteria: the f
                                                                                                                                                                                                                                                                                                                                                                                                                                      MYCOBACTERIUM SMEGMATIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA;
ACTINOMYCETALES; CORYNEBACTERINEAE; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete Sequence and Gene Organization of the Genome of Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii DNA RES. 5:55-76(1998)
                                                                                                   01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 62.8 KD PROTEIN.
                                                                                                                                                              066695
                                                                                                                                                                                                                                                                                                MOL. MICROBIOL. 14:557-569(1994).
EMBL; U10425; G595404; -.
PFAM; PF00551; formyl_transf; 1.
SEQUENCE 360 AA; 41130 MW; A81D7F3B.CRC32;
                                                                                                                                                   066695;
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-MC6
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 MEDLINE; 98196666.
DECKERT G., WARREN P.V.,
GRAHAM D.E., OVERBEEK R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 98344137
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                                     STRAIN-VF5
                                             SEQUENCE FROM N.A
                                                                     BACTERIA;
                                                                             AQ_372.
AQUIFEX AEOLICUS
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                                                                                                                                                                                                                     241 RALSDPYPNAYTY
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larity 53.88;
Conservative
                                                                                                                                                              PRELIMINARY;
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AA; 37168
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38.5%;
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                                                                   AQUIFICACEAE;
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  GAASTERLAND T., YOUNG W.G., LENOX A.L., SNEAD M.A., KELLER M., AUJAY M., HUBER
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Pred. No. 3
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                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A; ACTINOBACTERIDAE; MYCOBACTERIACEAE; M
                                                                    AQUIFEX
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3.20e+00;
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Matches
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Best Local
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MEDLINE; 92260626.
MARTINEZ M.A. DOPAZO J., I
DOMINGO E., KNOWLES N.J.;
"Evolution of the capsid pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q01124
Q01124;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
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PFAM; PF
COAT PRO
NON_TER
DOMAIN
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HYPOTHETICAL PROTEIN.
SEQUENCE 531 AA; 62830 MW; 585EBE7E CRC32;
                                                                                                                                                              DOMAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                          Substitutions over six decades.";

J. VIROL. 66:3557-3565(1992).

-:- THE COAT PROTEIN VP1 CONTAINS THE MAIN ANTIGENIC DETERMINANTS THE VIRION; THEREFORE, CHANGES IN ITS SEQUENCE MUST BE RESPONSIBLE FOR THE HIGH ANTIGENIC VARIABILITY OF THE VIRUS.
-:- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS, EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP3, AND VP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOOT-AND-MOUTH DISEASE VIRUS (APHTHOVIRUS C).
VIRUSES; SSRNA POSITIVE-STRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-VF5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COAT PROTEIN VP1
                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APHTHOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 TLKNRLENPYTF
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                                                                                                                                                                                                                                                                                VP3, AND VP4.
L; M90377; G210394;
M; PF00073; rhv; 1.
                                        RVLATRYTGTTTY
                                                                                                                                                                                                                                                                     PROTEIN.
  RTLNNRYTGPYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigenic variation without
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5 (TREMBLREL. 01, 1
} (TREMBLREL. 08, I
N VP1 (FRAGMENT).
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211 AA;
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larity 53.8%;
Conservative
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genome of t
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Pred.
1; M
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                               Score 58; DB 14; L
Pred. No. 4.88e+00;
1; Mismatches 5;
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                                                                                                                                                                                                         ANTIGENIC A
ANTIGENIC C
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                                                                                                                                                                  B1B474E6
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bacterium Aquifex
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                                                                                   Gaps
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53.2%;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative

    PRELIMINARY;

                                                CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 TLNGQYASPYLY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   720 KALVNRYRSPYS 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TLNNRYIGPYTF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::| ||| :||:
3 RTLNNRYIGPYT 14
                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                      STRAIN-N2;
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Q07117 .
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  CE-FKH-1
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1D 07
DD 07
DD 01
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                                                                                                                                                                                     SEQUENCE FROM N.A.

STAANN-VC-16 / DSM 4304 / ATCC 49558;

KEDINE; 98049343.

A KEDKN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

A KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

A RICHARDSON D.L., KERTAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

A RICHARDSON D.L., KERTAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

A RICHARDSON D.L., KERTAYAGE A.R., GADAS M.D., LOFTUS B.,

RIKNNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,

A PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU I.,

OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,

A OVERBEEK R., GOCAYNE J.D., WEIDMAN C., FUJII C., GARLAND S.A.,

A MASON P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

NEMBER R., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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BACTERIA; CYANOBACTERIA; NOSTOCALES; NOSTOCACEAE; ANABAENA
                                                                                              ARCHAEOGLOBUS FULGIDUS.
ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
ARCHAEOGLOBUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 1; Length 332;
Pred. No. 4.88e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58; DB 2; Length 444; Pred. No. 4.88e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; NATURE 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEALN-PCC 7120;

J., SCAPPINO L.A., HASELKORN R.;

JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

J5; G1195622;

J48; oxidored_nitro; 1.

444 AA; 48332 MW; 9C962756 CRC32;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UFDATE)
LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 AA; 38386 MW; 6844D7B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
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                      01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATIO)
NITRATE REDUCTASE, GAMMA SUBUNIT, PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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244145;
01-100-1996 (TREMBLREL. 01, CR
01-100-1996 (TREMBLREL. 01, LA
01-100-1998 (TREMBLREL. 01, LA
NIFN.
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017381 PRELIMINARY;
017381 017381
01-NOV-1996 (TREMBLREL. 01, C.
01-NOV-1996 (TREMBLREL. 01, L.
01-AUG-1998 (TREMBLREL. 07, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001069; G2650124; -.
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cal Similarity 46.2%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.2%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 AARILEDRFNIPY 257
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1 SARTLNNRYTGPY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENTER J.C.
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ID OIL
AC OIL
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DT 01
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Gaps
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SUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 87.2 KD PROTEIN
HYPOTHETICAL 87.2 KD PROTEIN
BARLEX STRIPE MOSAIC VIRUS (BSMV)
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; HORDEIVIRUS.
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KOZLOY YU.V., AFANAS'EV B.N., KUPASOV V.V.; GOLOVA YU.B.,
KULAEVA O.I., DOLYA V.V., ATABEKOV I.G., BAEV A.A.;
"Primary structure of RNA 3 of barley stripe mosaic virus and its
variability.";
                                                                                                                                                                                                                                                                                                               AZZARIA M., GOSZCZYNSKI B., CHUNG M.A., KALB J.M., MCGHEE J.D.;
SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.2%; Score 58; DB 5; Length 506; Best Local Similarity 50.0%; Prèd. No. 4.88e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MORTIMORE B.;
SUBMILLORE B.;
SUB
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VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.88e+00;
atches 2;
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PROSITE; PS00657; FORK_HEAD_1; 1.
SEQUENCE 500658; FORK_HEAD_2; 1.
SEQUENCE 506 AA; 55426 MW; 54119AA3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           770 AA; 87176 MW; 34477E66 CRC32;
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076025
076025
01.NOV-1996 (TREMBLREL. 01, CREATED)
01.NOV-1996 (TREMBLREL. 01, LAST SEQI
01.NOV-1999 (TREMBLREL. 01, LAST SEQI
01.NOV-1999 (TREMBLREL. 03, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. BIOL. MOSK. 23:1080-1090(1989).
EMBL: X52774; G297555; -.
PFAM; PF00978; RNA_dep_RNApol2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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accession
#title Conservation of structure and expression of the c-yes and fyn
genes in lower vertebrates.
#cross-references MUID:91187435
#accession 151592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
##residues 1-183,'S',185-436,'R',438-537 ##label KAWl
##residues 1-183,'S',185-436,'R',438-537 ##label KAWl
##cross references GB:M14676; NID:g338227; PID:g338228
##note the authors translated the codon GAA for residue 265 as
gln and GGA for residue 278 as gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawakami, T.; Pennington, C.Y.; Robbins, K.C.
Mol. Cell. Biol. (1986) 6:4195-4201
Isolation and oncogenic potential of a novel human src-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVHUSY #type complete protein-tyrosine kinase (EC 2.7.1.112) fyn, splice form B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *authors Kawakami, T.; Kawakami, Y.; Aaronson, S.A.; Robbins, K.C. #journal Proc. Natl. Acad. Sci. U.S.A. (1988) 85:3870-3874 #title Acquisition of transforming properties by FYN, a normal SRC-related human gene. #cross-references WID:88234523 #accession 159120
                                                                                                                                                                                                                                                   #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Semba, K.; Nishizawa, M.; Miyajima, N.; Yoshida, M.C.; Sukegawa, J.; Yamanashi, Y.; Sasaki, M.; Yamamoto, T. Toyoshima, K. Toyoshima, K. Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5459-5463 #file yer-related protooncogene, syn, belongs to the protein-tyrosine kinase family.
                                                                                                                                                                                                                                                                                                                                                  #domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN
#length 537 #molecular-weight 60447 #checksum 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                   ##molecule_type mRNA
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 2; Length 537; Pred. No. 1.04e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #residues 1-537 ##label SEM
#cross-references GB:M14333; NID:g181171; PID:g181172
                                                                                                                                                                              ##cross-references EMBL:X54971; NID:g64481; PID:g64482
                                                                                                                                                                                                                                                                                                                         #domain SH3 homology #label SH3
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514-522 ##label KAWZ
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#accession A25389
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larity 57.1%;
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##cross-references GB:M20284; NID:g182842; PID:g182843
##experimental_source clone pFYN(c)-11; termination mutant p56(fyn)

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*superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology alternative Splicing; ATP; autophosphorylation; blocked amino end; lipoprotein; monomer, myristylation; phosphoprotein; phosphotransferase; proto:oncogene; thiolester bond; transforming protein; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noble, M.E.M.; Musacchio, A.; Saraste, M.; Courtneidge, S.A.;
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#domain SH2 homology #label SH2\
...#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#modified_site myristylated amino end (GLy) (in mature form) #status predicted\
                                                                                                                                                                                                                                                                                                                                                                                             #authors Noble, M.; Musacchio, A.; Saraste, M.; Wierenga, R. stubmission submitted to the Brookhaven Protein Data Bank, May 1993 #cross-references PDB:1SHF #contents annotation; X-ray crystallography, 1.9 angstroms, residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *authors Morton, C.J.; Pugh, D.J.R.; Campbell, I.D. *submission submitted to the Brookhaven Protein Data Bank, April 1996 #consereferences PDB:INYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Musacchio, A.; Saraste, M.; Wilmanns, M.
Mature Struct. Biol. (1994) 1:546-551
High.resolution crystal structures of tyrosine kinase SH3
domains complexed with proline-rich peptides.
                                                                                                                                ##experimental_source clone pFYN(c)-2j; recombinant mutant p57(fyn)
NCE A58826
                                                                                                                                                                                   Peters, D.J.; McGrew, B.R.; Perron, D.C.; Liptak, L.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #Journal Dacogene (1990) 5:1313-1319
#title In vivo phosphorylation and membrane association of proto-oncogene product in IM-9 human lymphoblasts.
                                                                                                                                                                                                                                                                                                                                         annotation; myristylation; Tyr-531 phosphorylation A51398
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                                                                                                                                  #accession
                                                                                                                                              #authors Arhin, F.F.; Vining, L.C.
#journal Gene (1993) 126:129-133
#title Organization of the genes encoding p-aminobenzoic
#synthetase from Streptomyces lividans 1326.
#cross-references_MUID:93231526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
##residues 1-1
                                                                ##residues 1-475 ##label ARH
##cross-references GB:M64859; NID:g153393; PID:g153394
This enzyme participates in p-aminobenzoic acid biosynthesis.
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gene m3 protein - Lactococcus phage bIL170
#formal_name Lactococcus phage bIL170
24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
24-Mar-1999
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T03369
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ilarity 60.0%;
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#superfamily anthranilate synthase component I carbon-carbon lyase; oxo-acid-lyase; p-aminobenzoate
                                                                                                                                                                                                                                                            #formal_name Streptomyces lividans
14-Jul-1994 #sequence_revision 14.
21-Aug-1998
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p-Aminobenzoic acid synthetase (EC 4.1.3.-)
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#binding_site phosphate (Tyr) (covalent) (by
autophosphorylation) #status predicted\
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#journal Nucleic Acids Res. (1989) 17:4388
#title The glycinin Gy(3) gene from soyb
#cross-references MUID:89296500
                                                                                                                                                                                                                            #authors Nielsen, N.C.; Dickinson, C.
Scallon, B.J.; Fischer, R.
Goldberg, R.B.
#journal Plant Cell (1989) 1:313-328
#title Characterization of the glyo
#cross-references MUID:92393391
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##residues 1-484 ##label
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51.5%;
Similarity 58.3%;
7; Conservative
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glycinin G3 precursor - soybean
#formal_name Glycine max #common_name soybean
21-Nov-1993 #sequence_revision 19-Jan-1996 #te
03-May-1996
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96/1; 177/3; 352/3
#superfamily glycinin
#length 481 #molecular-weight 54241
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                                                  #domain signal sequence #status predicted #label #product glycinin G3 #status predicted #label MAT #length 484 #molecular-weight 54359 #checksum 8616
                                                                                                             storage protein
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Pred. No.
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Pred. No. 6.80e+00;
4; Mismatches 4
Score 51; DB 2;
Pred. No. 6.80e+00
2; Mismatches
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Best Local Similarity 58.3%;
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107-317
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*The complete nucleotide sequence of soybean glycinin A2B1a
gene spanning to another glycinin gene AlaB1b.
*cross-references_MUID:90332420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 481-495 ##label KIT
##cross-references EMBL:X53404; NID:g18522; PID:g18523
The source of this protein was cotyledon tissue taken 38 days after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-495 ##label NEG
##cross-references GB:X02985; NID:g18614; PID:g18615
##exper1mental_source cv. Bonminori
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            $10851 #type complete
glycinin Gl precursor - soybean
glycinin AlaBx
glycinin chain Ala; glycinin chain Bx
#formal_name Glycine max #common_name soybean
21-Nov-1993 #sequence_revision 19-Jan-1996 #text_change
08-Sep-1997
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Nucleic Acids Res. (1985) 13:6719-6731
A CDNA clone encoding a glycinin A-la subunit
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11S globulin; glycinin AlaBx
#formal_name Glycine max #common_name soybean
31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
S10851; S04603; JS0015
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#disulfide_bonds #status predicted
#th 495 #molecular-weight 55506 #checksum 8518
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#product glycinin chain Ala #status predicted #label
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Pred. No. 6.80e+00;
2; Mismatches 3
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Search completed: Fri Jun 11 17:58:45 1999 Job time: 83 secs.

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#journal Plant Cell (1989) 1:313-328
#title Characterization of the glycinin gene family in soybean.
#cross-references MUID:92393391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors. Sims, T.L.; Goldberg, R.B.
#journal Nucleic Acids Res. (1989) 17:4386
#title The glycinin Gy(1) gene from soybean.
#cross-references MUID:89296498
#accession S04603
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                     318 TMRLRHNIGQTS 329
                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
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Local Similarity 58.3%;
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#experimental_source variety Dare
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96/1; 180/3; 366/3
#superfamily glycinin
storage protein
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J. Agric. Food Chem. (1987) 35:210-214
An alternate cDNA encoding glycinin Ala Bx subunit.
                                                                                                                                              #product glycinin Bx chain *status predicted *label MAT3
#length 495 *molecular-weight 55706 *checksum 7917
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Scallon, B.J.; Fischer, R.L.;
                                                                          Conservative
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#product glycinin Gl #status predicted #label MATI\
#product glycinin Ala chain #status predicted #label
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                                                                        Score 51; DB 2; I
Pred. No. 6.80e+00;
2; Mismatches 3
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Sims, T.L.; Drews, G.N.;
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[MA]

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MPsrch_pp protein · protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:52:22 1999; MasPar time 2.45 Seconds 172.968 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-7
Description: (1-15) from US08991628.pep
Perfect Score: 9

Sequence: 1 QSGTMRTRHSTGGTN 15

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 24.516; Variance 27.383; scale 0.895

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

· 3222206876654321	Result
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5
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FAB1_YEAST	TERM_ADE12	TCPH_MOUSE	CATB_PSEAE	AMY_BACLI	NRAM_IAWHM	NRAM_IATRA	NRAM_IARUE	NIFN_RHISN	FILA_HUMAN	ACD_MYCLE	MAF2_MOUSE	S61B_ARATH	RS8_MAIZE	TIAM_HUMAN	TIAM_MOUSE	COPA_YEAST	C2TA_HUMAN	PHYA_POPTM	CAPP_ANANI	CC15_SCHPO	NARB_SYNP7
PROBABLE PHOSPHATIDYLI	DNA TERMINAL PROTEIN (T-COMPLEX PROTEIN 1, E	CATALASE PRECURSOR (EC	ALPHA-AMYLASE PRECURSO	NEURAMINIDASE (EC 3.2.	NEURAMINIDASE (EC 3.2.	NEURAMINIDASE (EC 3.2.	NITROGENASE IRON-MOLYB	FILAGGRIN PRECURSOR (F	ACYL-COA DEHYDROGENASE	TRANSCRIPTION FACTOR M	PROTEIN TRANSPORT PROT	40S RIBOSOMAL PROTEIN	T-LYMPHOMA INVASION AN	T-LYMPHOMA INVASION AN	COATOMER ALPHA SUBUNIT	MHC CLASS II TRANSACTI	PHYTOCHROME A.	PHOSPHOENOLPYRUVATE CA	CELL DIVISION CONTROL	NITRATE REDUCTASE (EC
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ALIGNMENTS

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EMBL; M76482; G190752; PIR; A41088; IJHUG3. MIM; 169615; PROSITE; PS00232; CADHERIN; 3. PRAM; PF00028; Cadherin; 4. PRAM; PF00028; Cadherin; 4.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	(POTENTIAL). (POTENTIAL). (POTENTIAL): (POTENTIALLY LETHAL SKIN FASULT OF THE AGAINST DSG3. (POTENTIALLY LETHAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIALLY LETHAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIALLY LETHAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIALLY LETHAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIALLY LETHAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIALLY LETHAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. (POTENTIAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE LOSS OF CELL-CELL ADHESION CAUSED BY THE AGAINST DSG3. (POTENTIAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE LOSS OF CELL-CELL ADHESION CAUSED BY AGAINST DSG3. (POTENTIAL SKIN FASULT OF THE LOSS OF CELL-CELL ADHESION CAUSE	MEDLINE; 92069753. MEDLINE; 92069753. AMAGAI M., KLAUS-KOVTUN V., STANLEY J.R.; "Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion."; CELL 67:869-877(1991). -i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. -i- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, OESOPHAGUS AND CARCINOMAS.	LT 1 DGG3_HUMAN STANDARD; PRT; 999 AA. P32926; 01-OCT-1993 (REL. 27, CREATED) 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DESMOGLEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA). DSG3. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

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                                                                 This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  01-AUG-1992
01-AUG-1992
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                            SOL_DROME P27398;
FLYBASE; FBgn0003464; sol.

PROSITE; PS00139; THIOL_PROTEASE_CYS;
PROSITE; PS00639; THIOL_PROTEASE_HIS;
PROSITE; PS00640; THIOL_PROTEASE_ASN;
PFAM; PF00641; zf-RanBP; 6.
                                                                                                                                                                                      brain gene of Drosophila melanogaster.";
PROC. NATL. ACAD. SCI. U.S.A. 88:7214-7218(1991).
-!- THE SOL (SMALL OPTIC LOBES) MUTATION ELIMINATES CERTAIN CLASSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
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                                          EMBL; M64084; G158483; -. PIR; A41146; BVFFSL.
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                                                                                                                                                                                                                                                                                       DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                 Molecular cloning and analysis of small optic lobes, a structural
                                                                                                                                                                                                                             MIKLOS G.L.G.;
                                                                                                                                                                                                                                    MEDLINE; 91334436.
DELANEY S.J., HAYWARD
                                                                                                                                                                                                                                                     TISSUE-BRAIN;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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ALTERNATIVE PRODUCTS:
IS OBSERVED, IN WHICH
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THE FIRST 393 ARE IDENTIC
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Pred. No. 4.
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Best Local
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01-DEC-1992 ()
01-DEC-1992 ()
15-DEC-1998 ()
DNA-DIRECTED
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ZN_FING
ZN_FING
DOMAIN
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MEDINE: 93077138.

KAUFMANN J., KLEIN A.;

"Gene dosage as a possible major determinant for equal expression

"Gene dosage as a possible major determinant for equal expression

levels of genes encoding RNA polymerase subunits in the hypotrichous

ciliate Euplotes octocarinatus.";

NUCLEIC ACIDS RES. 20:4445-4450(1992).

-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
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                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
  PFAM; PF00623; RNA_pol_A;
TRANSFERASE; DNA-DIRECTED
                                                                     EMBL;
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EUKARYOTA; ALVEOLATA; CILIOPHORA; HYPOTRICHS;
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THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRE POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED TWELVE DIFFERENT POLYPEPTIDES. THIS POLYPEPTIDE IS
                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TWELVE DIFFERENT POLYPEPTIDES. COMPONENT OF RNA POLYMERASE II.
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                                            S33886; S33886.
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RNA POLYMERASE II LARGEST SUBUNIT
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POLYMERASE; TRANSCRIPTION; ZINC; REPEAT;

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PROSITE; PS00107; PROTEIN
PROSITE; PS00109; PROTEIN
PROSITE; PS50011; PROTEIN
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
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Q05876;
01-FEB-1994
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ZN_FING
NON_TER
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EUKARYOTA; METAZOA; CHORDATA;
NEOGNATHAE; GALLIFORMES; PHAS
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                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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01-FEB-1994 (REL.
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                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: THYMUS AND SPLEEN.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE PHOSPHATE. SUBUNIT: ASSOCIATES THROUGH
                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP +
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European Bioinformatics Institute. There are no rest
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                                                                                                                                         PS50001; SH2; 1.
PS50002; SH3; 1.
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GREULICH H., NEM....
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68 8
478 4'
478 AA;
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1
2
81
148
267
                                                                                MYRISTYLATION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                        TRANSFERASE;
                                                                                                                                                              PROTEIN_KINASE_TYR;
PROTEIN_KINASE_DOM;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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inase, Yrk,
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PHASIANIDAE; PHASIANINAE; GALLUS
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Pred. No.
3; Misma
         BY SIMILARITY.
MYRISTATE (BY 9
PALMITATE (BY 9
PALMITATE (BY 9
SH3.
SH2.
                                                                               TYROSINE-PROTEIN KINASE;
SH3 DOMAIN; SH2 DOMAIN; PA
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 PROTEIN KINASE
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2.09e-01;
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SIMILARITY).
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                             MEDLINE: 97345356.
WOLVEN A., OKAMURA H., ROSENBLATT WOLVEN A., OKAMURA H., ROSENBLATT WOLL A CONTROL OF PS STATE OF THE PROPERTY OF THE PROPE
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MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;

EUKARYOTA; METAZOA; CHORDATA; MURIDAE; MURINAE;
               "Multiple features of the p59fyn src homology 4 domain for immune-receptor tyrosine based activation motif (IT and for plasma membrane localization.";

J. CELL BIOL. 133:1007-1015(1996).

1- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.

-1- CATALYTIC ACTYLITY: ATP + A PROTEIN TYROSINE - ADP PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 94019312.
SHENOY-SCARIA A.M., TIMSON L.K., KWONG J., SHAW A.S., LISHENDY-SCARIA A.M., TIMSON L.K., KWONG J., SHAW A.S., LIPALINE AND ADDRESS OF A MAINO-TERMINAL CYSTEINE MOTIF OF PI PAINT AND ADDRESS OF A MAINO-TERMINAL CELL. BIOL. 13:6385-6392(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC
                                                                                                                                             MEDLINE: 96251668.
GAUEN L.K.T., LINDER M.E.,
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95071286.
KOEGL M., ZLATKINE
"Palmitoylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COOKE M.P., PERLMUTTER R
"Expression of a novel f
hematopoietic cells.";
NEW BIOL. 1:66-74(1989).
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J. 303:749-753(1994)
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EMBL/GENBANK/DDBJ
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ATP (BY SIMILARITY).
BY SIMILARITY.
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PHOSPHORYLATION (BY SIMILARITY).
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DATA BANKS.
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a homologous
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Best Local :
Matches
SEQUENCE FROM N.A.

MEDLINE; 90191723.

STEELE R.E., DENG J.C., GHOSN C.R.

"Structure and expression of fyn g
ONCOGENE 5:369-376(1990).

-!- FUNCTION: IMPLICATED IN THE CC.

-!- CATALYTIC ACTIVITY: ATP + A PF
PROTEIN TYROSINE PHOSPHATE.

-!- SUBUNIT: ASSOCIATES THROUGH IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A44991; A44991.

MGD; MGI:95602; FYN.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1

PROSITE; PS50001; PROTEIN_KINASE_DOM; 1

PROSITE; PS50001; SH2; 1.

PROSITE; PS50001; SH2; 1.

PROSITE; PS500017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     PEAM; PE00017; SH2; 1.
PEAM; PE00018; SH3; 1.
PEAM; PE00059; pkinase; 1
HSSP; P06241; IFYN.
PROTO--NEO------
                                                                                                                                                                  FYN_XENLA
P13406;
                                                                                                                                                                                                                                                                                               DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                          01-JAN-1990 (REL. 13, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOY-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      TIPID
TIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                           MESOBATRACHIA;
                                                                                                   XENOPUS LAEVIS (AFRICAN CLAWED FROG) EUKARYOTA; METAZOA; CHORDATA; VERTEB
                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                 71 HTGTLRTRGGTGVT
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SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
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Similarity 57.1%;
8; Conservative
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533
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                                            GHOSN C.F
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MYRISTATE.
PALMITATE.
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ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred.
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CREENERS
         STRAIN-RIO LANCETILLA:
MEDILINE; 91187435.
HANNIG G., OTTILIE S., SCHAR
"Conservation of structure a
in lower vertebrates.";
ONCOGENE 6:361-369(1991).
                                                                                                                                                                                                        P27446;
01-AUG-1992
01-FEB-1994
01-OCT-1996
                                                                                                                                    EUKARYOTA;
TELEOSTEI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS50001; SH2; 1.

PROSITE; PS50002; SH3; 1.
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PIR; A43806;
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SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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SIMILARITY: COUTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
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f; PF00018; SH3; 1.
f; PF00069; pkinase; 1
p; P06241; 1FYN.
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PROSITE; PS00109; F
PROSITE; PS50011; F
PROSITE; PS50001; S
PROSITE; PS50002; S
SEQUENCE FROM N.A.
MEDLINE, 86287278.
SEMBA K., NISHIZAWA M., MIYA.
YAMANASHI Y., SASAKI M., YAM.
"Yes-related protooncogene, ikinase family.";
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PFAM; PF00069; pkinase; 1.
HSSP; P06241; 1AOT.
PROTO-ONCOGENE; TRANSFERASE;
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC
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PS50001; SH2; 1.
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SEQUENCE FROM N.A.
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MEDLINE: 87089775.
KAWAKAMI T., PENNINGTON C.Y., ROBBINS K.
KAWAKAMI T., PENNINGTON DOTENTIAL OF A
FINANCE OF THE CONTROL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYRISTOYLATION, AND PHOSPHORYLATION AT TYR-530.
MEDLLNE; 91016431.
PETERS D.J., MCGREW B.R., PERRON D.C., LIPTAK L.M., LAUD!
"In vivo phosphorylation and membrane association of the oncogene product in IM-9 human lymphoblasts.";
ONCOGENE 5:1313-1319(1990).
                                                                                                                                                                                                                                                                                 MEDLINE; 97121261.
RENZONI D.A., PUGH D.J., SILIGARDI G., DAS P., WATERFIELD M.D., CAMPBELL I.D., LADBURY J.E.;
"Structural and thermodynamic characterization the SI3 domain from Fyn with the proline-rich k subunit of PI3-kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROC.
                                                                                                                                                           "The SH2 domain from the tyrosine kinase F phosphotyrosyl peptide reveals insights in binding specificity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "High-resolution crystal structures of complexed with proline-rich peptides."; NAT. STRUCT. BIOL. 1:546-551(1994).
phosphatidylinositol 3-kinase in T cells.";
PROC. NATL. ACAD. SCI. U.S.A. 90:7366-7370(1993).
-i- FUNCTION: INCLICATED IN THE CONTROL OF CELL GRC
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMPBELL I.D.;
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MORTON C.J., PUGH
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"Crystal structure of the a
a Src family SH3 domain.";
CELL 85:931-942(1996).
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MEDLINE; 96279837.
LEE C.H., SAKSELA K.,
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EMBO J. 12:2617-2624(1993)
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                                                                                                    PRASAD
                                                                                                                                 BINDING OF
                                                                      NUDD C.E.;
                                                                                                                MEDLINE;
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Matches
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PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
PROTO-ONCOGENE; TRANSFERASE; TYROS
ATP-BINDING; MYRISTYLATION; SH3 DC
LIPOPROTEIN; 3D-STRUCTURE.
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STRAND
STRAND
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EMBL; M14676; G338228;
PIR; A24314; TVHUSY.
PIR; A25389; TVHUSR.
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               Local Similarity les 8; Consei
  71 HTGTLRTRGGTGVT
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SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: PHOSPHATI
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1NYF; 08-NOV-96.
1NYG; 08-NOV-96
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PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                    PS00107; PROTEIN_KINASE_ATP;
PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
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               Score 55; DB 1;
Pred. No. 3.54e-01
4; Mismatches
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BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
PHOSPHORYLATION.
A -> S (IN REF. 2).
A -> R (IN REF. 2).
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PALMITATE
PALMITATE
SH3.
SH2.
                                                                                                                                                                                                                                                                 TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; SH3 DOMAIN; SH2 DOMAIN; PALMITATE;
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ATP (BY SIMILARITY).
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                                              01B18DD0 CRC32;
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Query Match
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PROSITE; PS00751; 1
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PROSITE; PS00995; 1
PFAM; PF00118; cpnf
PFAM; PF00118; cpnf
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SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF
-I- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF
-I- FUNCTION: MOLECULAR TO PLAY A ROLE, IN VITRO, IN T
-ACTIN AND TUBULIN (BY SIMILARITY).

-I- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 9
FORMS TWO STACKED RINGS, 12 TO 16 MM IN DIAMETER (BY
-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCPH_HUMAN STANDARD; PRT; 543 AA.

(99832; O1487];
01-NOV-1997 (REL. 35, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1
INTERACTING PROTEIN).
CCT7 OR CCTH OR NIP7-1.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
PABB_STRLI STANDARD; PRT; 475 AA. P27630; 01-AUG-1992 (REL. 23, CREATED) 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. WON K.-A., REED S.I.; SUBMITTED (NOV-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 13-424 FROM N.A. FUKUSHI M., KIMURA T., YAMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF026292; G2559010; -. EMBL; U83843; G1800303; -.
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TCP1_2; 1.
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36, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) (HIV-1
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L -> P (IN REF. 2).
A -> P (IN REF. 2).
C -> L (IN REF. 2).
LRG -> SPC (IN REF. 2).
A -> P (IN REF. 2).
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Pred. No. 1.67e+00;
3; Mismatches 1.
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4.1.3.-) (ADC SYNTHASE).

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SEQUENCE FROM N.A.
STRAIN-CV. DARE; TISSUE-LEAF;
MEDLINE; 89296498.
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Best Local Similarity 58.3%;
Matches 7; Conservative
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STRAIN-CV. BONMINORI;
MEDLINE; 86041867.
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381 AA;
DISULFIDE BOND
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P04776;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIYCTNE MAX (SOYBEAN).
GIXBARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
                                                         NIELSEN N.C., DICKINSON C.D., CHO T.-J., THANH V.H., SCALLON B.J., FISCHER R.L., SIMS T.L., DREWS G.N., GOLDBERG R.B.; "Characterization of the glycinin gene family in soybean."; PLANT CELL 1:313-328(1989).
-i- FUNCTION: GLYCLIN IS THE MAJOR SEED STORAGE PROTEIN OF SOYBEAN.
-i- SUBBUNIT: HEXAMER; EACH SUBBNIT IS COMPOSED OF AN ACIDIC AND A BASIC CHAIN DERIVED FROM A SINGLE PRECURSOR AND LINKED BY A
                                                                                                                                                                                                                                                                                                                                                                              Gaps
         STREPTOMYCES LIVIDANS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLC3_SOYBN STANDARD; PRT; 481 AA.
P118728;
01-0CT-1989 (REL. 12, CREATED)
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLYCININ G3 PRECURSOR [CONTAINS: GLYCININ A SUBUNIT; GLYCININ B
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Pred. No. 2.76e+00;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                    475 AA; 52042 MW; 9A70C557 CRC32;
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STRAIN-CV, DARE; TISSUE-LEAF;
MEDLINE; 89296500.
CHO T.-J., NIELSEN N.C.;
"The glycinin Gy3 gene from soybean.";
NUCLDIC ACIDS RES. 17:4388-4388(1989).
                                                                                                                                                                                                                                                                                                               PFAM; PF00425; chorismate_bind; 1.
LYASE; FOLATE BIOSYNTHESIS.
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Best Local Similarity 42.9%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  281 AGTLRGRPRAGGDD 294
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                                                   SEQUENCE FROM N.A.
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
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-i - SIMILARITY: BELONGS TO THE 11S SEED STORAGE PROTEINS (GLOBULINS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLYCININ G1 PRECURSOR (CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX
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SEQUENCE FROM N.A.
MEDILINE; 92393391.
NIELSEN N.C., DICKINSON C.D., CHO T.J., THANH V.H., SCALLON B.J.,
NIELSEN K.L., SIMS T.L., DREWS G.N., GOLDBERG R.B.;
FICHER R.L., STANS T.L., DREWS G.N., GOLDBERG R.B.;
PLARACTERIZATION of the glycinin gene family in soybean.";
PLANT CELL 1:313-328(1989).
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Pred. No. 2.76e+00;
2; Mismatches 3; Indels
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54241 MW; BlA5BDFO CRC32;
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UTSIMI S., KOHNO<sup>™</sup>M., MORI T., KITO'M.;
"An alternate cDMA encoding glycinin Ala Bx subunit.";
"A. AGRIC. FOOD CHEM. 35:210-214(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X15123; G18639; -.
PIR; S04605; S04605.
PROSITE; PS001305; 11S_EED_STORAGE; 1.
SEED STORAGE PROTEIN; MULTIGENE FAMILY; SIGNAL.
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B SUBUNIT.
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"The glycinin Gyl gene from soybean.";
NUCLEIC ACIDS RES. 17:4386-4386(1989).
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Best Local S
Matches
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EMBL; X15121; G18635; -.
EMBL; X02985; G18615; -.
PIR; A23497; FWSYG2.
PIR; S04603; S04603.
PIR; S04603; S04603.
PIR; S10851; S10851.
                                                                                                                                                                                                                                MA5D_SCHJA
P13411;
01-JAN-1990
C1-JAN-1990
15-JUL-1998
                               MEDLINE; 89261924.

SCALLON B.J., BOGITSH B.J., CARTER C.E.;

SCALLON B.J., BOGITSH B.J., CARTER C.E.;

"Characterization of a large gene family in Schistosoma jap

that encodes an immunogenic miracidial antigen.";

MOL. BICCHEM. PARASITOL. 33:105-112(1989).

-I- DEVELOPMENTAL STAGE: MIRACIDIA.

-I- SIMILARITY: NEARLY IDENTICAL TO IMMUNOGENIC MIRACIDIAL

ANTIGENS 81', 81 AND 8C.
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STRAIN-PHILIPPINE;
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                                                                                                                                                                      SCHISTOSOMATOIDEA;
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                                                                                                                                                                                                                      MMUNOGENIC
                                                                                                                                                                                                                                                                                                                                             318 TMRLRHNIGQTS
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- SUBUNIT: HEXAMER; EACH
- SASIC CHAIN DERIVED ID DISULFIDE BOND.
- PIM: THE PRECURSOR IS
                                                                                                                                                                                                                                                                                                                                4 TMRTRHSTGGTN 15
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SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                   A JAPONICUM (BLOOD FLUKE).
METAZOA; PLATYHELMINTHES;
ATOIDEA; SCHISTOSOMATIDAE;
                                                                                                                                                                                                                    (REL. 13, C)
(REL. 13, L)
(REL. 36, L)
MIRACIDIAL
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llarity 58.3%;
Conservative
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ROTEIN; MULTIGENE FAMILY; SIGNAL.
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L ANTIGEN 5D (FRAGMENT).
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Pred. No. 2.76e+00;
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SCHISTOSOMA
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P06167;
01-JAN-1988
01-JAN-1988
01-OCT-1996
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                                                                                                                                                                                                                                                         EMBL;
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
01-APR-1993 (REL. 27, LAST ANNOTATION UPDATE)
AMINOCIYCOSIDE N3'-ACETYLTRANSFERASE TYPE VII
CAMINOCYCLITOL 3-N-ACETYLTRANSFERASE TYPE VII
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ANTIGEN; MULTIGENE FAMILY.
NON_TER 1 1
                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-siborsend an email to license@isb-sib.ch).
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MEDLINE; 91285425.
SALAUZE D., PEREZ-GONZALEZ J.A., PIEPERSBERG W., DAVIES J.;
"Characterisation of aminoglycoside acetyltransferase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREPTOMYCES FRADIAE.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCES
                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: RESISTANCE TO NEOMYCIN.
-i- CATALYTIC ACTIVITY: ACETYL-COA + A 2-DEOXYSTREPTAMINE
- COA + N3'-ACETYL-2-DEOXYSTREPTAMINE ANTIBIOTIC.
-i- SIMILARITY: TO OTHER AAC(3) PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENE 101:143-148(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of neomycin-producing Micromonospora
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286 AA; 30455
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llarity 38.5%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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MEDLINE; 87174819.

SUZU S., SAKAI Y., SHIDDA T., SHIBUTA H.;

NUCLEOCTIDE sequence of the bovine parainfluenza 3 v1rus genome: the genes of the F and HN glycoproteins.";

NUCLEIC ACIDS RES. 15:2945-2958(1987).

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEUROAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMNINIC ACID CONTAINING
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS N-TERMINAL HYDROPHOBIC SEQUENCE.
-1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOVINE PARAINFLUENZA 3 VIRUS.
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; MONONEGAVIRALES;
PARAMYXOVIRIDAE; PARAMYXOVIRINAE; PARAMYXOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y00114; G60897; -..
EMBL; D84095; G1255658; -.
PIR; B27218; HNNZB3.
PFAM; PF00423; HN; 1.
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18 GTTRDRHSSKATN 30
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3 GTMRTRHSTGGTN 15
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572 AA;
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EXTRACELLULAR (POTENTIAL).
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Pred. No. 4.53e+00;
2; Mismatches 3; Indels
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 11 17:54:53 1999; MasPar time 6.10 Seconds 134.225 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-991-628-7 (1-15) from US08991628.pep 99 QSGTMRTRHSTGGTN 15

Scoring table: РАМ 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% ... Listing first 45 summaries

Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 24.193; Variance 26.150; scale 0.925

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	PARTIAL CDS.	RYANODINE RECEPTOR.				KIAA0440 (FRAGMENT).	MAJOR SURFACE GLYCOPRO	PRECURSOR.	HISTOCOMPATIBILITY 2,	RPKA.	NOD L.	HEMAGGLUTININ-NEURAMIN	CEPHALOSPORIN C HYDROX	T06D8.3 PROTEIN.	VIRULENCE PROTEIN.		GLYCOPROTEIN B:	COSMID H22D07.	w	W	GLYCOPROTEIN B	w	w	B	ŭ

ALIGNMENTS

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STRAIN-A3(2);
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01-AUG-1998
01-NOV-1998
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"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOL. MICROBIOL. 21:77-96(1996).
EMBL; AL031514; E1319225; -.
SEQUENCE 421 AA; 44174 MW; 7B444909 CRC32;
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DE COUET H.G., FONG K.S., WEEDS A.G., MCLAUGHLIN P.J., MIKLOS "MOLECULAR and multational analysis of a gelsolin-family member encoded by the flightless I gene of Drosophila melanogaster."; GENETICS 141:1049-1059(1995).
                                                                  MALESZKA R., DE COUET H.G., MIKLOS G.L.G:;
PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
EMBL; AF01777; G3004662; -.
SEQUENCE 1597 AA; 174696 MW; C6C4952E
                                                                                                                                              MIKLOS G.L., YAMAMOTO M., BURNS R.G., MALESZKA R.; "An essential cell division gene of Drosophila, absent from Saccharomyces, encodes an unusual protein with tubulin-like myosin-like peptide motifs."; PROC. NATL. ACAD. SCI. U.S.A. 94:5189-5194(1997).
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-CANTONS;
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EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
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Q62844;
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EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                 NEMOTO K., SEKIMOTO M., KAGEYAMA H., FUKAN UEYAMA T., SENBA E., TOMITA I.; SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ EMBL; U35365; G1101768; -
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-NOV-1998 (TREMBLREL. 08,
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SEQUENCE 534
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PFAM; PF00018; SH3; 1.
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PROSITE; PS00109;
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                                                                                                                                                                  PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
SEQUENCE 537 AA; 60701;
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SHRSP STROKE-PRONE SPONTANEOUSLY HYPERTENSIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHO!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTO-ONCOGENE FYN.
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EMBL; S74774; G802051; -
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                                                                                                                                                                                                                                                                                                                                                                            TISSUE-WHOLE BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A
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                                                                                   h 55.6%;
Similarity 57.1%;
8; Conservative
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534 AA; 60226
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PROTEIN_KINASE_TYR;
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AE; MURINAE; RATTUS.
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Pred. No.
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OKANO M., XIE S., LI E.;

"Cloning and characterization of a factorization of a factoriz
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OKANO M., XIE S., LI E.;

"Cloning and characterization of a f:

"Cytosine-5) methyltransferases.";

NAT. GENET. 19:219-220(1998).

EMBL; AFO68627; G3327982; -

TRANSFERASE; METHYLTRANSFERASE.

SEQUENCE 839 AA; 94798 MW; BD2AD
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MUS MUSCULUS
EUKARYOTA; ME'
DIMITIB.
MUS MUSCULUS (MOUSE)
TOWARYOTA; METAZOA;
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MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VE
                                                                                                 01-NOV-1998 (TREMBLREL 08, CREATED)
01-NOV-1998 (TREMBLREL 08, LAST SEQ
01-NOV-1998 (TREMBLREL 08, LAST ANN
01-NOV-1998 (TREMBLREL 38)
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O88510;
O1-NOV-1998 (TREMBLREL 08, CREATED)
O1-NOV-1998 (TREMBLREL 08, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
DNA_CYTOSINE-5 METHYLTRANSFERASE 3B2.
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01-NOV-1998 (TREMBLREL. 08, LAST
01-NOV-1998 (TREMBLREL. 08, LAST
DNA CYTOSINE-5 METHYLTRANSFERASE
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1 QSGTMRTRHSTGGTN 1
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QSGTMRTRHSTGGTN 15
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Similarity 46.7%;
7; Conservative
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METAZOA; CHORDATA; VERTEBRATA;
HT: MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                   PRELIMINARY;
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                    CHORDATA;
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SEQUENCE FROM N.A.

MEDILINE; 98324766.

OKANO M., XIE S., LI E.;

CANO M., XIE S., LI E.;

COLONING and characterization of a (cytosine-5) methyltransferases.";

NAT. GENET. 19:219-220(1998).

EMBL; AF068626; G3327980; -.

TRANSFERASE; METHYLTRANSFERASE.

SEQUENCE 859 AA; 97232 MW; AECI
                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE; 95325326.

BIDNENKO E., EHRLICH D., CHOPIN M.C.;

"Phage operon involved in sensitivity to abortive infection mechanism AbiD1.";

abortive infection mechanism AbiD1.";

BACTERIOL. 177.3824-3829(1995).

EMBL; L35175; G845551; "...

EMBL; L35175; G845551; "...
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SEQUENCE
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HYPOTHETICAL PROTEIN.
SEQUENCE 160 AA; 17990 MW; 9D027B4F CRC32;
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01-JAN-1998 (TREMBLREL 05, L
01-JAN-1998 (TREMBLREL 05, L
HYPOTHETICAL 18.0 KD PROTEIN.
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BACTERIOPHAGE 712.
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MIDDLE EXPRESSED M1, M2,
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RINCE A., FITZGERA
INFLUENZA A VIRUS
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Identification of a DNA region
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6; Conservative
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Pred. No.
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No. 1.33e+00;
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| AbiF; I
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EMBL; U85989; G1835742; -
FFAM; PF00064; neur; 1
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044476;
044476;
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EMBL; U85988; G1835740; -.
PFAM; PF00064; neur; 1.
SEQUENCE 469 AA; 51888 MW; 3FB1AOA5 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P88838;
                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                        CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                  01-JUN-1998 (TREMBLREL. 06, 01-JUN-1998 (TREMBLREL. 06, 01-NOV-1998 (TREMBLREL. 08, 204A4.4 PROTEIN.
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01-MAY-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
           WILSON R., AINSCOUGH R., BONFIELD J., BURTON J., CRAXTON M., DEAR S., DU
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VIRUSES; SSRNA NEGATIVE-STRAND
INFLUENZA VIRUS A AND B GROUP.
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MEDLINE; 97335203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; ORTHOMYXOVIRIDAE; INFLUENZA VIRUS A AND B GROUP.
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A/EQUINE/PRAGUE/1/56;
MEDLINE; 97335203.
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                                                                                                                                                                                                                                        1 QSGTMRTRHSTGGTN 15
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46.7%;
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   HAWKINS
  , ANDERSON K., BAYNES C., CONNELL M., COPSEY T., CO., DURBIN R., FAVELLO A AWKINS T., HILLIER L., JI
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03,
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Pred. No. 1.33e+00;
4; Mismatches 4
                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred.
4; }
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uenza A virus o
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luenza A virus of
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C., BERKS M.,
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, JIER M., JOHI
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RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMUTRAY A., MORTINGRE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., MORTINGRE D., O'CALLAGHAN M.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SHOWNKEEN R.,
RA THIERY.MIEG J., THOMAS K., VADDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.", C., WILKINSON-SPROAT J., WOLLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.", C., WOLLDMANN P., BIEWALD T.;
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA SAMMONS L., WOHLDMANN P., BIEWALD T.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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RN SUBMITTED (DE-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN SUBMITTED (DE-1997)
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